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09/818943 Eriksson et al. 3/28/01

SEQ ID NO: 1 and 2
1) interference search

Thank you,

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NA#: _____ AA#: _____
Interference: _____ SPDI: _____
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Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

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OM protein - protein search, using sw model

Run on: September 3, 2005, 19:08:39 ; Search time 118.5 Seconds
(without alignments)
1126.011 Million cell updates/sec

Title: US-09-818-943-1
Perfect score: 1858
Sequence: 1 MSFLGLLVTSALAQRRGT.....DVALEHHBCDCVCRGSTGG 345

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1858	100.0	345	3	AAY84557
2	1858	100.0	345	5	AAE13212
3	1858	100.0	345	8	ADR31425
4	1851	99.6	345	2	AAY41766
5	1851	99.6	345	2	AAY30023
6	1851	99.6	345	2	AAY33679
7	1851	99.6	345	3	AB33414
8	1851	99.6	345	3	AB19578
9	1851	99.6	345	3	AB10651
10	1851	99.6	345	3	AB10633
11	1851	99.6	345	3	AB10650
12	1851	99.6	345	3	AB10635
13	1851	99.6	345	3	AB10644
14	1851	99.6	345	3	AB24432
15	1851	99.6	345	3	AB24412
16	1851	99.6	345	3	AAV59285
17	1851	99.6	345	3	AAV96858
18	1851	99.6	345	3	AB48657
19	1851	99.6	345	3	AB401419
20	1851	99.6	345	3	AB24250
21	1851	99.6	345	3	AAE02649
22	1851	99.6	345	4	AAU12314
23	1851	99.6	345	4	AB53074
24	1851	99.6	345	4	AB74028
25	1851	99.6	345	4	AB65603

26	1851	99.6	345	4	AAU08465	Aau08465 Polypteti
27	1851	99.6	345	4	AAB50980	Aab50980 Human PRO
28	1851	99.6	345	4	AAB49895	Aab49895 Human PRO
29	1851	99.6	345	4	AAE00997	Aae00997 Human zve
30	1851	99.6	345	5	ABB79884	Abb79884 Human vas
31	1851	99.6	345	5	ABG92889	Abg92889 Human VEG
32	1851	99.6	345	5	AAB47889	Aab47889 Human zve
33	1851	99.6	345	5	ABB81331	Abb81331 Human VEG
34	1851	99.6	345	5	AAU76684	Aau76684 Human zve
35	1851	99.6	345	6	ABO17758	Abol17758 Novel hum
36	1851	99.6	345	6	ABU72434	Abu72434 Human ZVE
37	1851	99.6	345	6	ABO25268	Abol25268 Novel hum
38	1851	99.6	345	6	ABU81012	Abu81012 Human PRO
39	1851	99.6	345	6	ABU72274	Abu72274 Novel hum
40	1851	99.6	345	6	ABU66712	Abu66712 Human PRO
41	1851	99.6	345	6	ABU84954	Abu84954 Human sec
42	1851	99.6	345	6	ABG72132	Abg72132 Human vas
43	1851	99.6	345	6	ABU59793	Abu59793 Novel sec
44	1851	99.6	345	6	ABU61152	Abu61152 Human PRO
45	1851	99.6	345	6	ABO24983	Abol24983 Human sec

ALIGNMENTS

RESULT 1
AAY84557
ID AAY84557 standard; protein, 345 AA.
AC AAY84557;
XX
DT 25-JUL-2000 (first entry)
XX
DE Amino acid sequence of platelet-derived growth factor C (PDGF-C).
XX
KW Platelet-derived growth factor C; PDGF-C; cell proliferation;
KW growth factor; heparin; connective tissue; wound healing; VEGF-F;
KW fibroblast mitogenesis; PDGF alpha receptor activation; tumour growth;
KW choriocarcinoma; Wilms tumour; megakaryoblastic leukaemia;
KW lung carcinoma; erythroleukemia; tissue remodelling.
XX
OS Homo sapiens.
XX
FN WO200018212-A2.
XX
PD 06-APR-2000.
XX
PF 30-SEP-1999; 99WO-US022668.
XX
PR 30-SEP-1998; 98US-0102461P.
PR 12-NOV-1998; 98US-0108109P.
PR 03-DEC-1998; 98US-0110749P.
PR 18-DEC-1998; 98US-0113002P.
PR 21-MAY-1999; 99US-0135426P.
PR 15-JUL-1999; 99US-0144022P.
XX
(LUDWIG-) LUDWIG INST CANCER RES.
(UYHE-) UNIV HELSINKI LICENSING LTD.
XX
PA Eriksson U, Aase K, Lee X, Ponten A, Uutela M, Alitalo K;
FI Oestman A, Heldin C, Betsholz C;
XX
DR WPI; 2000-292954/25.
DR N-PSDB; AAA12523.
XX
PT Novel DNA encoding PDGF-C useful to stimulate or enhance proliferation,
PT differentiation, growth and motility of cells expressing the PDGF-C
PS receptor.
XX
PS Claim 27; Fig 2; 135pp; English.
XX
CC The present sequence represents human platelet-derived growth factor C
CC (PDGF-C) (formally designated VEGF-F). PDGF-C polypeptides have the

CC ability to stimulate and enhance proliferation or differentiation, and/or
 CC growth or motility of cells expressing a PDGF-C receptor. PDGF-C
 CC polypeptides can be used in pharmaceuticals for promoting cell
 CC proliferation, preferably in combination with one other growth factor and
 CC heparin. Pharmaceuticals comprising PDGF-C polypeptides can also be used
 CC for stimulating connective tissue or wound healing. The PDGF-C
 CC polypeptide can be enzymatically processed to generate the active
 CC truncated form of PDGF-C and used to regulate the receptor-binding
 CC specificity of PDGF-C. PDGF-C can also be used to promote fibroblast
 CC mitogenesis in a mammal and to induce PDGF alpha receptor activation.
 CC PDGF-C antagonists can be used to inhibit tumour growth of a tumour
 CC expressing PDGF-C in a mammal. Specific types of human tumours, e.g.
 CC choriocarcinoma, Wilms tumour, megakaryoblastic leukaemia, lung carcinoma
 CC and erythroleukemia, can be identified by testing for expression of PDGF-
 CC C. PDGF-C antagonists can also be used to inhibit tissue remodeling
 CC during invasion of tumour cells into a normal population of cells.
 CC Antagonists can also be used to treat fibrotic conditions, especially
 CC found in the lung, kidney or liver
 XX
 SQ Sequence 345 AA;

Query Match 100.0%; Score 1858; DB 3; Length 345;
 Best Local Similarity 100.0%; Pred. No. 6.2e-179;
 Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSLFGLLLVTSALAGRRGTQAESNLSSKFQSSNKQNGVQDPQHERIITVSTNGSIHS 60
 DB 1 MSLFGLLLVTSALAGRRGTQAESNLSSKFQSSNKQNGVQDPQHERIITVSTNGSIHS 60
 QY 61 PRFPHYPRNTVLVRLVAEENVMWQLTDFRFGLEDPEDDICKYDFVEEPEPSDGTIL 120
 DB 61 PRFPHYPRNTVLVRLVAEENVMWQLTDFRFGLEDPEDDICKYDFVEEPEPSDGTIL 120
 QY 121 GRWCGSGTVPGKQISKGNIQIRFVSDEYFPSEPGFCIHYNIMVMPQFTEAVSPVLPPSA 180
 DB 121 GRWCGSGTVPGKQISKGNIQIRFVSDEYFPSEPGFCIHYNIMVMPQFTEAVSPVLPPSA 180
 QY 181 LPLDLLNNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
 DB 181 LPLDLLNNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
 QY 241 LTEEVRVLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPFSK 300
 DB 241 LTEEVRVLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPFSK 300
 QY 301 VTKKYHEVLQRLPKTGVRGLHKSITDVALEHHEECDCVCRGSTGG 345
 DB 301 VTKKYHEVLQRLPKTGVRGLHKSITDVALEHHEECDCVCRGSTGG 345

RESULT 2
 AAE13212
 ID AAE13212 standard; protein; 345 AA.
 AC AAE13212;
 XX
 DT 12-FEB-2002 (first entry)
 XX
 DE Human platelet-derived growth factor (PDGF-C) protein.
 XX
 KW Human; transgenic animal; platelet derived growth factor C; PDGF-C;
 KW cardiac hypertrophy; fibrosis.
 XX
 OS Homo sapiens.
 XX
 PN WO200172132-A1.
 XX
 PD 04-OCT-2001.
 XX
 PF 28-MAR-2001; 2001WO-US009855.
 XX
 PR 28-MAR-2000; 2000US-0192507P.
 XX

PA (LUDW-) LUDWIG INST CANCER RES.
 XX Eriksson U, Li X, Ponten A, Aase K, Li H;
 XX WPI; 2002-010700/01.
 DR
 XX A transgenic animal over-expressing platelet derived growth factor C is
 PT useful to study and find therapy for disease associated with PDGF-C over-
 PT expression, including cardiac hypertrophy and fibrosis.
 PS Disclosure; Page 40-42; 48pp; English.
 XX
 CC The patent discloses a method for producing a transgenic, non-human
 CC animal over-expressing a platelet derived growth factor C (PDGF-C), or
 CC its functional fragment or analogue. The method involves introducing a
 CC transgenic PDGF-C DNA into a cell of a non-human animal, introducing the
 CC cell into a non-human animal and allowing the cell to develop into a
 CC transgenic, non-human animal. The transgenic animal is useful as a model
 CC to study disease states characterised by over-expression of PDGF-C and to
 CC find therapy for those diseases, particularly hypertrophy and fibrosis in
 CC various organs including the heart. The present sequence is PDGF-C
 CC protein from human
 XX
 SQ Sequence 345 AA;

Query Match 100.0%; Score 1858; DB 5; Length 345;
 Best Local Similarity 100.0%; Pred. No. 6.2e-179;
 Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSLFGLLLVTSALAGRRGTQAESNLSSKFQSSNKQNGVQDPQHERIITVSTNGSIHS 60
 DB 1 MSLFGLLLVTSALAGRRGTQAESNLSSKFQSSNKQNGVQDPQHERIITVSTNGSIHS 60
 QY 61 PRFPHYPRNTVLVRLVAEENVMWQLTDFRFGLEDPEDDICKYDFVEEPEPSDGTIL 120
 DB 61 PRFPHYPRNTVLVRLVAEENVMWQLTDFRFGLEDPEDDICKYDFVEEPEPSDGTIL 120
 QY 121 GRWCGSGTVPGKQISKGNIQIRFVSDEYFPSEPGFCIHYNIMVMPQFTEAVSPVLPPSA 180
 DB 121 GRWCGSGTVPGKQISKGNIQIRFVSDEYFPSEPGFCIHYNIMVMPQFTEAVSPVLPPSA 180
 QY 181 LPLDLLNNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
 DB 181 LPLDLLNNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
 QY 241 LTEEVRVLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPFSK 300
 DB 241 LTEEVRVLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPFSK 300
 QY 301 VTKKYHEVLQRLPKTGVRGLHKSITDVALEHHEECDCVCRGSTGG 345
 DB 301 VTKKYHEVLQRLPKTGVRGLHKSITDVALEHHEECDCVCRGSTGG 345

RESULT 3
 ADR31425
 ID ADR31425 standard; protein; 345 AA.
 AC ADR31425;
 XX
 DT 04-NOV-2004 (first entry)
 XX
 DE Human platelet derived growth factor C (PDGF-C) protein.
 XX
 KW VEGF; vascular endothelial growth factor; PDGF;
 KW platelet derived growth factor; gene therapy; myelosuppression;
 KW ischaemia; human.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT Domain
 FT /note = CUB domain of PDGF-C

FT	Domain	164..345	AC	AAY41766;
FT	FT	/note = Minimal domain	XX	
XX	WO2004070018-A2.		DT	07-DEC-1999 (first entry)
PN			XX	Human PRO200 protein sequence.
XX	19-AUG-2004.		DE	
PD			XX	
XX	04-FEB-2004; 2004WO-US003316.		KW	Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
PF	04-FEB-2003; 2003US-0445021P.		KW	probe; blood coagulation disorder; cancer; cellular adhesion disorder;
XX	04-FEB-2003; 2003US-0471412P.		KW	secreted protein; transmembrane protein.
PR	16-MAY-2003; 2003US-0471412P.		XX	
XX	(LUDW-) LUDWIG INST CANCER RES.		OS	Homo sapiens.
PA	(LICN) LICENTIA LTD.		XX	
PA	(UYFL-) FLANDERS INTERUNIVERSITY INST BIOTECHNOL.		XX	WO9946281-A2.
XX			PD	16-SEP-1999.
XX			XX	
PI	Alitalo K, Eriksson U, Carmeliet P, Li X, Collen D;		PF	08-MAR-1999; 99WO-US005028.
PI	Yla-Herttuala S, Salven P, Rajantie R;		XX	
XX			XX	10-MAR-1998; 98US-0077450P.
DR	WPI; 2004-604438/58.		PR	11-MAR-1998; 98US-0077632P.
DR	N-PSDB; ADR31424.		PR	11-MAR-1998; 98US-0077641P.
XX			PR	11-MAR-1998; 98US-0077649P.
XX			PR	12-MAR-1998; 98US-0077791P.
PT	Stimulating stem cell recruitment, proliferation, or differentiation to		PR	13-MAR-1998; 98US-0078004P.
PT	stimulate myelopoiesis by vascular endothelial growth factor B or		PR	17-MAR-1998; 98US-00040220.
PT	platelet derived growth factor therapy.		PR	20-MAR-1998; 98US-0078886P.
XX			PR	20-MAR-1998; 98US-0078910P.
PS	Claim 51; SEQ ID NO 7; 151pp; English.		PR	20-MAR-1998; 98US-0078936P.
XX			PR	20-MAR-1998; 98US-0078939P.
CC	The present invention relates to a method of stimulating stem cell		PR	25-MAR-1998; 98US-0079294P.
CC	recruitment, proliferation, or differentiation to stimulate myelopoiesis		PR	26-MAR-1998; 98US-0079656P.
CC	by vascular endothelial growth factor B (VEGF-B) product or platelet		PR	27-MAR-1998; 98US-0079663P.
CC	derived growth factor (PDGF) therapy. The invention is useful in gene		PR	27-MAR-1998; 98US-0079664P.
CC	therapy and for treating myeloapression and ischaemia. The invention is		PR	27-MAR-1998; 98US-0079689P.
CC	also useful for manufacturing a medicament for mobilizing endothelial		PR	27-MAR-1998; 98US-0079728P.
CC	progenitor cells to the peripheral blood in a mammalian subject. The		PR	27-MAR-1998; 98US-0079786P.
CC	present sequence is human platelet derived growth factor C (PDGF-C)		PR	30-MAR-1998; 98US-0079920P.
CC	protein. This sequence is used to illustrate the method of invention.		PR	30-MAR-1998; 98US-0079923P.
XX			PR	31-MAR-1998; 98US-0080105P.
SQ	Sequence 345 AA;		PR	31-MAR-1998; 98US-0080107P.
			PR	31-MAR-1998; 98US-0080156P.
	Query Match 100.0%; Score 1858; DB 8; Length 345;		PR	31-MAR-1998; 98US-0080194P.
	Best Local Similarity 100.0%; Fred. No. 6.2e-179;		PR	01-APR-1998; 98US-0080327P.
	Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		PR	01-APR-1998; 98US-0080328P.
QY	1 MSLFGLLVTSALAGRGRTQAESNLSSKFQFSSNKEQNGVDPQHERIITVSTNGSIHS 60		PR	01-APR-1998; 98US-0080333P.
Db			PR	01-APR-1998; 98US-0080334P.
	1 MSLFGLLVTSALAGRGRTQAESNLSSKFQFSSNKEQNGVDPQHERIITVSTNGSIHS 60		PR	08-APR-1998; 98US-0081049P.
			PR	08-APR-1998; 98US-0081070P.
QY	61 PRPPTYPRNTVLVRLVAEENVVMIQLTDFDERFGLDEPDDICKYDFVEVEEPSDGTIL 120		PR	08-APR-1998; 98US-0081071P.
Db			PR	09-APR-1998; 98US-0081195P.
	61 PRPPTYPRNTVLVRLVAEENVVMIQLTDFDERFGLDEPDDICKYDFVEVEEPSDGTIL 120		PR	09-APR-1998; 98US-0081203P.
			PR	09-APR-1998; 98US-0081229P.
QY	121 GRWCSSGTVPGQISKGQIRIRFVSDYFPPSEPGFCIHYNIWMPQFTEAVSPSVLPESA 180		PR	15-APR-1998; 98US-0081817P.
Db			PR	15-APR-1998; 98US-0081838P.
	121 GRWCSSGTVPGQISKGQIRIRFVSDYFPPSEPGFCIHYNIWMPQFTEAVSPSVLPESA 180		PR	15-APR-1998; 98US-0081952P.
			PR	15-APR-1998; 98US-0081955P.
QY	181 LPDLLNNAITAFSTLEDLIRLPERWQDLEDYRPTWQLGKAFVFGKRSRVVDLNL 240		PR	21-APR-1998; 98US-0082568P.
Db			PR	21-APR-1998; 98US-0082569P.
	181 LPDLLNNAITAFSTLEDLIRLPERWQDLEDYRPTWQLGKAFVFGKRSRVVDLNL 240		PR	22-APR-1998; 98US-0082700P.
			PR	22-APR-1998; 98US-0082704P.
QY	241 LTEEVRVLSCTPRNFVSISIRELKRDTIFWPGLLVKRCGNACCLHNCNECQVPSK 300		PR	22-APR-1998; 98US-0082804P.
Db			PR	23-APR-1998; 98US-0082767P.
	241 LTEEVRVLSCTPRNFVSISIRELKRDTIFWPGLLVKRCGNACCLHNCNECQVPSK 300		PR	23-APR-1998; 98US-0082796P.
			PR	27-APR-1998; 98US-0083336P.
QY	301 VTKKYHEVLQLPKPTGVRGLHSLTDVALEHHEECDCVCRGSTGG 345		PR	27-APR-1998; 98US-0083342P.
Db			PR	29-APR-1998; 98US-0083392P.
	301 VTKKYHEVLQLPKPTGVRGLHSLTDVALEHHEECDCVCRGSTGG 345		PR	29-APR-1998; 98US-0083495P.
			PR	29-APR-1998; 98US-0083496P.
			PR	29-APR-1998; 98US-0083499P.
			PR	29-APR-1998; 98US-0083500P.
			PR	29-APR-1998; 98US-0083545P.
			PR	29-APR-1998; 98US-0083554P.
			PR	29-APR-1998; 98US-0083558P.

RESULT 4
AAY41766
ID AAY41766 standard; protein; 345 AA.
XX

```
PR 29-APR-1998; 98US-0083559P.
PR 30-APR-1998; 98US-0083742P.
PR 05-MAY-1998; 98US-0084366P.
PR 06-MAY-1998; 98US-0084414P.
PR 06-MAY-1998; 98US-0084441P.
PR 07-MAY-1998; 98US-0084598P.
PR 07-MAY-1998; 98US-0084600P.
PR 07-MAY-1998; 98US-0084627P.
PR 07-MAY-1998; 98US-0084637P.
PR 07-MAY-1998; 98US-0084639P.
PR 07-MAY-1998; 98US-0084640P.
PR 13-MAY-1998; 98US-0085323P.
PR 13-MAY-1998; 98US-0085338P.
PR 13-MAY-1998; 98US-0085339P.
PR 15-MAY-1998; 98US-0085573P.
PR 15-MAY-1998; 98US-0085579P.
PR 15-MAY-1998; 98US-0085580P.
PR 15-MAY-1998; 98US-0085582P.
PR 15-MAY-1998; 98US-0085689P.
PR 15-MAY-1998; 98US-0085697P.
PR 15-MAY-1998; 98US-0085700P.
PR 15-MAY-1998; 98US-0085704P.
PR 18-MAY-1998; 98US-0086023P.
PR 22-MAY-1998; 98US-0086392P.
PR 22-MAY-1998; 98US-0086414P.
PR 22-MAY-1998; 98US-0086430P.
PR 22-MAY-1998; 98US-0086486P.
PR 28-MAY-1998; 98US-0087098P.
PR 28-MAY-1998; 98US-0087106P.
PR 28-MAY-1998; 98US-0087208P.
PR 30-JUL-1998; 98US-0094651P.
PR 11-SEP-1998; 98US-0100038P.
XX
- PA
XX (GETH ) GENENTECH INC.
XX
PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
XX
DR WPI, 1999-551358/46.
DR N-PSDB; AAZ34296.
XX
PT New secreted and transmembrane polypeptides and their polynucleotides,
PT useful for treating blood coagulation disorders, cancers and cellular
PT adhesion disorders.
XX
PS Claim 12; Fig 207; 530pp; English.
XX
CC The present invention describes secreted and transmembrane polypeptides
CC and their polynucleotides. The nucleotide sequences are useful as sources
CC of probes, primers, for chromosome mapping, and for generation of
CC antisense sequences. They can also be used to create transgenic animals.
CC The proteins can be used to treat a variety of diseases and disorders,
CC depending on their function. Diseases that may be treated include blood
CC coagulation disorders, cancers and cellular adhesion disorders. They may
CC also be used to raise antibodies. AAZ33891 to AAZ3438, and AAY41685 to
CC AAY4174 represent polynucleotide and polypeptide sequence given in the
CC exemplification of the present invention
XX
SQ Sequence 345 AA;
Query Match 99.6%; Score 1851; DB 2; Length 345;
Best Local Similarity 99.4%; Pred. No. 3.1e-178;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSLFGLLLVTSALAGORGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60
DB 1 MSLFGLLLVTSALAGORGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60
QY 61 PRPHTYPRNTVLVRLVAEENVMVLTDFDRFGLDEPDICKYDFVEEPEPDSGTIL 120
DB 61 PRPHTYPRNTVLVRLVAEENVMVLTDFDRFGLDEPDICKYDFVEEPEPDSGTIL 120
QY 121 GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNVMPQTEAVSPSVLPFSA 180
DB 121 GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNVMPQTEAVSPSVLPFSA 180
QY 181 LPLDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKRSRVDNL 240
DB 181 LPLDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKRSRVDNL 240
QY 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPFSK 300
DB 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPFSK 300
QY 301 VTKKYHEVLQRLPKTGVRLGHLKSLTDVALEHHHEECDCVCRGSTGG 345
DB 301 VTKKYHEVLQRLPKTGVRLGHLKSLTDVALEHHHEECDCVCRGSTGG 345
XX
RESULT 5
AAAY30023
ID AAY30023 standard; protein; 345 AA.
XX
AC AAY30023;
XX
DT 11-OCT-1999 (first entry)
XX
DE Human vascular endothelial growth factor related protein.
XX
KW Vascular endothelial growth factor related protein; VEGF-R protein;
KW tissue growth inhibition; tumour growth; cancer; tissue growth;
KW angiogenesis; coronary artery blockage.
XX
OS Homo sapiens.
XX
PN WO9937671-A1.
XX
PD 29-JUL-1999.
XX
PF 26-JAN-1999; 99WO-US001574.
XX
PR 27-JAN-1998; 98US-0072635P.
PR 05-JUN-1998; 98US-0088089P.
PR 24-JUN-1998; 98US-0090544P.
PR 31-AUG-1998; 98US-0098548P.
XX
PA (ELIL ) LILLY & CO ELI.
XX
PI Dou S, Na S, Song HY;
XX
DR WPI; 1999-458680/38.
DR N-PSDB; AAX86352.
XX
PT A vascular endothelial growth factor related protein and related
XX polynucleotide, useful for identifying antagonists and binding compounds.
XX
PS Claim 1; Page 56-58; 62pp; English.
XX
CC The present sequence represents a vascular endothelial growth factor
CC related (VEGF-R) protein. VEGF-R can be used in assays to identify
CC antagonists that bind to it or that antagonize its activity. VEGF-R
CC antagonists (e.g. anti-VEGF-R antibodies) are useful for inhibiting
CC tissue growth. This is useful for inhibiting tumour growth and for
CC treating cancer. VEGF-R itself can be used to stimulate tissue growth,
CC angiogenesis and to treat coronary artery blockage. The VEGF-R coding
CC sequence can be used for the recombinant production of the VEGF-R protein
XX
SQ Sequence 345 AA;
Query Match 99.6%; Score 1851; DB 2; Length 345;
Best Local Similarity 99.4%; Pred. No. 3.1e-178;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSLFGLLLVTSALAGORGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60
DB 1 MSLFGLLLVTSALAGORGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60
QY 121 GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNVMPQTEAVSPSVLPFSA 180
DB 121 GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNVMPQTEAVSPSVLPFSA 180
```


XX WO2000053758-A2.
XX PD 14-SEP-2000.
XX PF
XX 02-MAR-2000; 2000WO-US005841.
XX 08-MAR-1999; 99WO-US005028.
XX 10-MAR-1999; 99US-0123618P.
XX 12-MAR-1999; 99US-0123957P.
XX 23-MAR-1999; 99US-0125775P.
XX 12-APR-1999; 99US-0128849P.
XX 20-APR-1999; 99WO-US008615.
XX 28-APR-1999; 99US-0131445P.
XX 04-MAY-1999; 99US-0132371P.
XX 14-MAY-1999; 99US-0134287P.
XX 02-JUN-1999; 99WO-US012252.
XX 23-JUN-1999; 99US-0141037P.
XX 20-JUL-1999; 99US-0144758P.
XX 26-JUL-1999; 99US-0145698P.
XX 28-JUL-1999; 99US-0146222P.
XX 01-SEP-1999; 99WO-US020111.
XX 08-SEP-1999; 99WO-US020594.
XX 13-SEP-1999; 99WO-US020944.
XX 15-SEP-1999; 99WO-US021090.
XX 15-SEP-1999; 99WO-US021547.
XX 05-OCT-1999; 99WO-US023089.
XX 29-OCT-1999; 99US-0162506P.
XX 29-NOV-1999; 99WO-US028214.
XX 30-NOV-1999; 99WO-US028313.
XX 30-NOV-1999; 99WO-US028409.
XX 01-DEC-1999; 99WO-US028301.
XX 01-DEC-1999; 99WO-US028634.
XX 02-DEC-1999; 99WO-US028551.
XX 02-DEC-1999; 99WO-US028564.
XX 02-DEC-1999; 99WO-US028565.
XX 16-DEC-1999; 99WO-US030095.
XX 20-DEC-1999; 99WO-US030999.
XX 30-DEC-1999; 99WO-US031274.
XX 05-JAN-2000; 2000WO-US000219.
XX 06-JAN-2000; 2000WO-US000277.
XX 06-JAN-2000; 2000WO-US000376.
XX 11-FEB-2000; 2000WO-US003565.
XX 18-FEB-2000; 2000WO-US004341.
XX 18-FEB-2000; 2000WO-US004342.
XX 22-FEB-2000; 2000WO-US004414.
XX (GETH) GENENTECH INC.
XX PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;
PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;
XX WPI; 2000-572271/53.
XX N-PSDB; AAC58579.
XX Sixty four PRO polypeptides, useful in the diagnosis and treatment of
PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid
PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus.
XX Claim 33; Fig 2; 309pp; English.
XX The present invention describes sixty four human PRO proteins which can
CC be used in the treatment of immune related diseases. The human PRO
CC proteins, anti-PRO antibodies, agonists and antagonists are useful for
CC treating and diagnosing immune related disorders. The disorders are
CC selected from systemic lupus erythematosus, rheumatoid arthritis,
CC osteoarthritis, juvenile chronic arthritis, spondyloarthritis,
CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,
CC immune-mediated renal disease, demyelinating diseases of the central and
CC peripheral nervous systems, hepatobiliary diseases, inflammatory bowel

CC disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune
CC or immune-mediated skin diseases, allergic diseases, immunological
CC diseases of the lung, and transplantation associated diseases including
CC graft rejection and graft-versus-host-disease. AAC58397 to AAC58578
CC represent PCR primers and hybridisation probes used in the isolation of
CC human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477
CC represent human PRO polynucleotide and protein sequences given in the
CC exemplification of the present invention
XX Sequence 345 AA;
SQ Query Match 99.6%; Score 1851; DB 3; Length 345;
Best Local Similarity 99.4%; Pred. No. 3.1e-178;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSLFGLLLVTSALAGORRGQAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS 60
DB 1 MSLFGLLLVTSALAGORRGQAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS 60
QY 61 PRFHTYPRNTLVWRLVAEENWVIOITDERFGLDEPDIDCKYDFVEEPESDGTIL 120
DB 61 PRFHTYPRNTLVWRLVAEENWVIOITDERFGLDEPDIDCKYDFVEEPESDGTIL 120
QY 121 GRWCGSGTVPGKQISKGNQIRIRFVSDEYFSEPGFCIHYNVMPQFTAEVSPSLPESA 180
DB 121 GRWCGSGTVPGKQISKGNQIRIRFVSDEYFSEPGFCIHYNVMPQFTAEVSPSLPESA 180
QY 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWOLGKAFVFGKRSRVVDLNL 240
DB 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWOLGKAFVFGKRSRVVDLNL 240
QY 241 LTEEVRVLYSCPTPNFVSIRIELARTDTIFWPGCLLVKRCGNCACCLHNCNEQCVPSPK 300
DB 241 LTEEVRVLYSCPTPNFVSIRIELARTDTIFWPGCLLVKRCGNCACCLHNCNEQCVPSPK 300
QY 301 VTKKYHEVLQRLPKTGVGRGLHSLTDVALEHHEECDCVCRGSTGG 345
DB 301 VTKKYHEVLQRLPKTGVGRGLHSLTDVALEHHEECDCVCRGSTGG 345
RESULT 8
AAB19578
ID AAB19578 standard; protein; 345 AA.
XX AC AAB19578;
XX DT 22-JAN-2001 (first entry)
XX DE Human PRO200 (vascular endothelial growth factor E).
XX KW PRO200; vascular epithelial growth factor E; VEGF-E; human;
KW ocular disease; retinopathy; maculopathy; therapy; retinitis pigmentosa;
KW macular degeneration; retinal detachment; retinal tear; macular hole;
KW myopia; traumatic choriorretinopathy; acute retinal necrosis syndrome;
KW contusion; edema; retinal vision occlusion; vascular disease;
KW retinal vasculitis; thrombocytopenic purpura; uveitis; retinal occlusion.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT Peptide 1. .14
FT Protein /label= Signal_peptide
FT /label= Mature_Pro200
FT Modified-site 15. .21
FT /note= "N-myristoylation"
FT Modified-site 25. .29
FT /note= "Asn is N-glycosylated"
FT Modified-site 55. .59
FT /note= "Asn is N-glycosylated"
FT Modified-site 117. .123
FT /note= "N-myristoylation"
FT Modified-site 127. .133

FT Modified-site /note= "N-myristoylation"
 FT 254..258
 FT Modified-site /note= "Asn is N-glycosylated"
 FT 281..287
 FT Modified-site /note= "N-myristoylation"
 FT 282..288
 FT Modified-site /note= "N-myristoylation"
 FT 319..325
 FT /note= "Amidation"
 XX
 PN WO200053760-A2.
 XX
 PD 14-SEP-2000.
 XX
 PF 10-MAR-2000; 2000WO-US006319.
 XX
 PR 12-MAR-1999; 99US-0123957P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ferrara N, Goddard A, Gurney AL, Hebert C, Henzel WJ;
 PI Kabakoff RC, Klein RD, Kijavini IJ, Kuo SS, La Fleur M, Wood WT;
 XX
 DR WPI: 2000-587437/55.
 DR N-PSDB; AAA88515.
 XX
 PT Novel PRO polypeptides useful for preventing or rescuing retinal cells
 PT from injury caused by ocular diseases such as retinitis pigmentosa,
 PT retinopathy, retinal degenerative diseases, degenerative myopia, uveitis.
 XX
 XX Claim 2; Fig 2; 140pp; English.
 PS
 CC The present sequence is that of human PRO200 or vascular endothelial
 CC growth factor E (VEGF-E), as predicted from a cDNA clone (see AAA88515)
 CC that was isolated from a glioma cell line G61 library using probes (see
 CC AAA88523-26) based on an expressed sequence tag (see AAA88522) that
 CC showed homology to VEGF. PRO200 has a predicted mol.wt. of 39,029 and a
 CC pI of about 6.06. A method for producing PRO polypeptides, including
 CC PRO200, using a host cell transformed with a vector comprising a PRO
 CC nucleic acid is claimed. The invention relates to the use of PRO
 CC polypeptides to delay, prevent or rescue retinal cells such as retinal
 CC neurons selected from photoreceptors, retinal ganglion cells, displaced
 CC retinal ganglion cells, amacrine cells, displaced amacrine cells,
 CC horizontal and bipolar neurons, and supportive cells (including Mueller
 CC cells and pigment epithelial cells) from injury and degradation. The
 CC retinal cells are preferably photoreceptors and photoreceptor cell injury
 CC or death is caused by retinal injury, light or environmental trauma or by
 CC an ocular disease selected from retinitis pigmentosa, macular
 CC degeneration, including age-related, retinal detachment, retinal tears,
 CC retinopathy, retinal degenerative diseases, macular holes, degenerative
 CC myopia, acute retinal necrosis syndrome, traumatic chorioretinopathies or
 CC confusion such as Purtscher's retinopathy, edema, ischemic conditions
 CC such as central or branch retinal vision occlusion, collagen vascular
 CC diseases, thrombocytopenic purpura, uveitis, retinal vasculitis and
 CC occlusion associated with Kales disease and systemic lupus erythematosus
 CC (claimed)
 XX
 SQ Sequence 345 AA;
 Query Match 99.6%; Score 1851; DB 3; Length 345;
 Best Local Similarity 99.4%; Pred. No. 3.1e-178;
 Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSLFGLLLVTSALAGQGRGTQAESNLSSKFQFSSNKEONGVQDPQHERIIITVSTNGSIHS 60
 DB 1 MSLFGLLLVTSALAGQGRGTQAESNLSSKFQFSSNKEONGVQDPQHERIIITVSTNGSIHS 60
 QY 61 PRFPHYPRNTVLVRLVAEENWVIQITFDERFGLEDPEDDICKYDFVEEPEPSDGTIL 120
 DB 61 PRFPHYPRNTVLVRLVAEENWVIQITFDERFGLEDPEDDICKYDFVEEPEPSDGTIL 120
 QY 121 GRWCGSGTVPGKQISKGNQIRIRFVSDYFSPSEPGFCIHYNVMPQFTEAVSPVLPSPA 180
 DB 121 GRWCGSGTVPGKQISKGNQIRIRFVSDYFSPSEPGFCIHYNVMPQFTEAVSPVLPSPA 180
 QY 181 LPDLNNAITAFSTLEDLIRYLEPERWQDLEDLIRPTWQLLGKAFVFGKRSRVVDLNL 240
 DB 181 LPDLNNAITAFSTLEDLIRYLEPERWQDLEDLIRPTWQLLGKAFVFGKRSRVVDLNL 240
 QY 241 LTERVRLYSCTPRNFSVSIREEELKRTDTIFWPGCLLVKRCGNCACCLHNCNECOCVPSK 300
 DB 241 LTERVRLYSCTPRNFSVSIREEELKRTDTIFWPGCLLVKRCGNCACCLHNCNECOCVPSK 300
 QY 301 VTKKYHEVLQLRPKTGVRGLHKSITDVALEHHEECDCVCRGSTGG 345
 DB 301 VTKKYHEVLQLRPKTGVRGLHKSITDVALEHHEECDCVCRGSTGG 345
 RESULT 9
 AAB10651
 ID AAB10651 standard; protein; 345 AA.
 XX
 AC AAB10651;
 XX
 DT 19-JAN-2001 (first entry)
 XX
 DE Human VEGF-X protein #3.
 XX
 KW VEGF-X; vascular endothelial growth factor; human; vulnery; cytostatic;
 KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
 KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
 KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
 KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
 KW venous sore; diabetic ulcer; burns; skin graft growth.
 XX
 OS Homo sapiens.
 XX
 SN WO2000037641-A2.
 XX
 PD 29-JUN-2000.
 XX
 PF 21-DEC-1999; 99WO-US030503.
 XX
 PR 22-DEC-1998; 98GB-00028377.
 PR 18-MAR-1999; 99US-0124967P.
 PR 08-NOV-1999; 99US-0164131P.
 XX
 PA (JANC) JANSEN PHARM NV.
 XX
 PI Gordon RD, Sprengel JJ, Yon JR, Dijkmans JH, Gosiewska A;
 PI Dhanaraj SN, Xu J;
 XX
 WIPI: 2000-442669/38.
 XX
 PT New vascular endothelial growth factor protein, useful for treating or
 PT preventing diseases associated with inappropriate angiogenesis activity
 PT such as cancer, rheumatoid arthritis, psoriasis and wounds.
 XX
 PS Claim 72; Fig 12; 127pp; English.
 XX
 CC This invention describes a novel vascular endothelial growth factor-X
 CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has
 CC vulnery, cytostatic, antirheumatic, antiarthritic, antipsoriatic and
 CC antidiabetic activity and acts as an angiogenesis and vascularization
 CC regulator. An antisense molecule of the invention is useful for treating
 CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
 CC retinopathy by inhibiting angiogenic activity or inappropriate
 CC vascularization including formation and proliferation of new blood
 CC vessels, growth and development of tissues, tissue regeneration and organ
 CC and tissue repair in a subject. The products of the invention are useful
 CC for preparing medicaments for treating wounds such as dermal ulcers,
 CC pressure sores, venous sores, diabetic ulcers and burns and to promote
 CC skin graft growth, tissue repair, proliferation of new blood vessels,
 CC tissue regeneration and organ repair by promoting angiogenic activity or
 CC vascularization. This sequence represents the human VEGF-X protein
 CC described in the method of the invention

```
XX SQ Sequence 345 AA;
Query Match 99.6%; Score 1851; DB 3; Length 345;
Best Local Similarity 99.4%; Pred. No. 3.1e-178;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSLFGLLLVTSALACQRRGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60
DB 1 MSLFGLLLVTSALACQRRGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60
QY 61 PRFPHTYPRNTVLVRLVAEENVWIQLTDFERFGLDEPDDICKYDFVEVEEPSDGTIL 120
DB 61 PRFPHTYPRNTVLVRLVAEENVWIQLTDFERFGLDEPDDICKYDFVEVEEPSDGTIL 120
QY 121 GRWCGSGTVPKGQISKGNQIRIRFVSDYFPEPFGFCIHYNIVMPQFTEAVSPVLPPSA 180
DB 121 GRWCGSGTVPKGQISKGNQIRIRFVSDYFPEPFGFCIHYNIVMPQFTEAVSPVLPPSA 180
QY 181 LPDLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGAFFGGRKSRVVDLNL 240
DB 181 LPDLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGAFFGGRKSRVVDLNL 240
QY 241 LTEEVRVLSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPK 300
DB 241 LTEEVRVLSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPK 300
QY 301 VTKKYHEVLQRPKTVGRGLHKSITDVALEHHEEDCVCVRGSGTG 345
DB 301 VTKKYHEVLQRPKTVGRGLHKSITDVALEHHEEDCVCVRGSGTG 345
RESULT 10
ID AAB10633
AC AAB10633;
XX
DT 19-JAN-2001 (first entry)
DE Human RACE generated VEGF-X protein.
XX
KW VEGF-X; vascular endothelial growth factor; human; vulnery; cytostatic;
KW antiarthritis; antipsoriatic; antidiabetic; treatment;
KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
KW venous sore; diabetic ulcer; burns; skin graft growth.
XX
OS Homo sapiens.
XX
PN WO200037641-A2.
XX
PD 29-JUN-2000.
XX
PF 21-DEC-1999; 99WO-US030503.
XX
PR 22-DEC-1998; 98GB-00028377.
PR 18-MAR-1999; 99US-0124967P.
PR 08-NOV-1999; 99US-0164131P.
XX
PA (JANC ) JANSSEN PHARM NV.
XX
PI Gordon RD, Sprengel JJ, Yon JR, Dijkmans JJH, Gosiewska A;
PI Dhanaraj SN, Xu J;
XX
DR WPI: 2000-442669/38.
DR N-PSDB; AAA71951.
XX
PT New vascular endothelial growth factor protein, useful for treating or
PT preventing diseases associated with inappropriate angiogenesis activity
PT such as cancer, rheumatoid arthritis, psoriasis and wounds.
XX
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PS Disclosure; Fig 6; 127pp; English.
XX
CC This invention describes a novel vascular endothelial growth factor-X
CC (VEGF-X) protein (Ia) and its encoding polynucleotide (Iia) which has
CC vulnery, cytostatic, antiarthritis, antipsoriatic, antidiabetic and
CC antiangiogenic activity and acts as an angiogenesis and vascularization
CC regulator. An antisense molecule of the invention is useful for treating
CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
CC retinopathy by inhibiting angiogenic activity or inappropriate
CC vascularization including formation and proliferation of new blood
CC vessels, growth and development of tissues, tissue regeneration and organ
CC and tissue repair in a subject. The products of the invention are useful
CC for preparing medicaments for treating wounds such as dermal ulcers,
CC pressure sores, venous sores, diabetic ulcers and burns and to promote
CC skin graft growth, tissue repair, proliferation of new blood vessels,
CC tissue regeneration and organ repair by promoting angiogenic activity or
CC vascularization. This sequence represents the RACE generated human VEGF-X
CC protein described in the method of the invention
XX
SQ Sequence 345 AA;
Query Match 99.6%; Score 1851; DB 3; Length 345;
Best Local Similarity 99.4%; Pred. No. 3.1e-178;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSLFGLLLVTSALACQRRGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60
DB 1 MSLFGLLLVTSALACQRRGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60
QY 61 PRFPHTYPRNTVLVRLVAEENVWIQLTDFERFGLDEPDDICKYDFVEVEEPSDGTIL 120
DB 61 PRFPHTYPRNTVLVRLVAEENVWIQLTDFERFGLDEPDDICKYDFVEVEEPSDGTIL 120
QY 121 GRWCGSGTVPKGQISKGNQIRIRFVSDYFPEPFGFCIHYNIVMPQFTEAVSPVLPPSA 180
DB 121 GRWCGSGTVPKGQISKGNQIRIRFVSDYFPEPFGFCIHYNIVMPQFTEAVSPVLPPSA 180
QY 181 LPDLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGAFFGGRKSRVVDLNL 240
DB 181 LPDLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGAFFGGRKSRVVDLNL 240
QY 241 LTEEVRVLSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPK 300
DB 241 LTEEVRVLSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPK 300
QY 301 VTKKYHEVLQRPKTVGRGLHKSITDVALEHHEEDCVCVRGSGTG 345
DB 301 VTKKYHEVLQRPKTVGRGLHKSITDVALEHHEEDCVCVRGSGTG 345
RESULT 11
AAB10650
ID AAB10650 standard; protein; 345 AA.
XX
AC AAB10650;
XX
DT 19-JAN-2001 (first entry)
DE Human 990126veg protein.
XX
KW VEGF-X; vascular endothelial growth factor; human; vulnery; cytostatic;
KW antiarthritis; antipsoriatic; antidiabetic; treatment;
KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
KW venous sore; diabetic ulcer; burns; skin graft growth.
XX
OS Homo sapiens.
XX
PN WO200037641-A2.
XX
PD 29-JUN-2000.
XX
```

```
PF 21-DEC-1999; 99WO-US030503.
XX
XX 22-DEC-1998; 98GB-00028377.
PR 18-MAR-1999; 99US-0124967P.
PR 08-NOV-1999; 99US-0164131P.
XX
XX (JANC ) JANSSEN PHARM NV.
XX
XX Gordon RD, Sprengel JJ, Yon JR, Dijkmans JJH, Gosiowska A;
PI Dhanaraj SN, Xu J;
XX
XX WPI; 2000-442669/38.
XX
XX New vascular endothelial growth factor protein, useful for treating or
PT preventing diseases associated with inappropriate angiogenesis activity
PT such as cancer, rheumatoid arthritis, psoriasis and wounds.
XX
XX Disclosure; Fig 11; 127pp; English.
XX
XX This invention describes a novel vascular endothelial growth factor-X
CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIfa) which has
CC vulnary, cytosatic, antirheumatic, antiarthritic, antipsoriatic and
CC antidiabetic activity and acts as an angiogenesis and vascularization
CC regulator. An antisense molecule of the invention is useful for treating
CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
CC retinopathy by inhibiting angiogenic activity or inappropriate
CC vascularization including formation and proliferation of new blood
CC vessels, growth and development of tissues, tissue regeneration and organ
CC and tissue repair in a subject. The products of the invention are useful
CC for preparing medicaments for treating wounds such as dermal ulcers,
CC pressure sores, venous sores, diabetic ulcers and burns and to promote
CC skin graft growth, tissue repair, proliferation of new blood vessels,
CC tissue regeneration and organ repair by promoting angiogenic activity or
CC vascularization. This sequence represents the human 990126vegX protein
CC used to illustrate the method of the invention
XX
XX Sequence 345 AA;
SQ
Query Match 99.6%; Score 1851; DB 3; Length 345;
Best Local Similarity 99.4%; Pred. No. 3.1e-178;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSLFGLLLVTSALAGORRGTQAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS 60
DB 1 MSLFGLLLVTSALAGORRGTQAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS 60
QY 61 PRFPHYPRNTVLRVLAVERNWIQLTFDERFGLDEPDICKYDFVEVEEPSDGTIL 120
DB 61 PRFPHYPRNTVLRVLAVERNWIQLTFDERFGLDEPDICKYDFVEVEEPSDGTIL 120
QY 121 GRWCGSGTVPGKQISKGNIQIRFVSDVEYFPSEPGFCIHYNVMPQFTAVSPSVLPSPA 180
DB 121 GRWCGSGTVPGKQISKGNIQIRFVSDVEYFPSEPGFCIHYNVMPQFTAVSPSVLPSPA 180
QY 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
DB 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
QY 241 LTEEVRVLSCTPRNSVSIRELKTDTIFWPGCLLVKRCGNACCLHNCNCCVPSK 300
DB 241 LTEEVRVLSCTPRNSVSIRELKTDTIFWPGCLLVKRCGNACCLHNCNCCVPSK 300
QY 301 VTKKHEVLQRPKTVGRGLHSLTDVALEHHEECDCVCRGSTGG 345
DB 301 VTKKHEVLQRPKTVGRGLHSLTDVALEHHEECDCVCRGSTGG 345
RESULT 12
AAB10635
ID AAB10635 standard; protein; 345 AA.
XX
AC AAB10635;
XX
```


Db 181 LPDLNNNAITAFSTLEDLIRYLEPERWQLDLEDLYRFTWQLLGKAFVFGKSRVVDLNL 240
QY 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300
Db 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300
QY 301 VTKKYHEVLQRPKTGVRGLHKS LTDVALEHHEECDCVCRGSTGG 345
Db 301 VTKKYHEVLQRPKTGVRGLHKS LTDVALEHHEECDCVCRGSTGG 345

RESULT 13

AAB10644

ID AAB10644 standard; protein; 345 AA.

XX AC AAB10644;

XX DT 19-JAN-2001 (first entry)

XX XX Human VEGF-X protein #4.

XX KW VEGF-X; vascular endothelial growth factor; human; vulnery; cytostatic;
XX KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
XX KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
XX KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
XX KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
XX KW venous sore; diabetic ulcer; burns; skin graft growth.

XX OS Homo sapiens.

XX XX WO200037641-A2.

XX PN 29-JUN-2000.

XX PD 21-DEC-1999; 99WO-US030503.

XX PF 22-DEC-1998; 98GB-00028377.

XX PR 18-MAR-1999; 99US-0124967P.

XX PR 08-NOV-1999; 99US-0164131P.

XX XX (JANC) JANSSEN PHARM NV.

XX XX Gordon RD, Sprengel JJ, Yon JR, Dijkmans JJH, Gosiowska A;

XX PI Dhanaraj SN, Xu J;

XX DR WPI; 2000-442669/38.

XX DR N-PSDB; AAA71990.

XX XX New vascular endothelial growth factor protein, useful for treating or

XX PT preventing diseases associated with inappropriate angiogenesis activity

XX PT such as cancer, rheumatoid arthritis, psoriasis and wounds.

XX PS Disclosure; Fig 30B; 127pp; English.

XX CC This invention describes a novel vascular endothelial growth factor-X
XX CC (VEGF-X) protein (Ia) and its encoding polynucleotide (Iia) which has
XX CC vulnery, cytostatic, antirheumatic, antiarthritic, antipsoriatic and
XX CC antidiabetic activity and acts as an angiogenesis and vascularization
XX CC regulator. An antisense molecule of the invention is useful for treating
XX CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
XX CC retinopathy by inhibiting angiogenic activity or inappropriate
XX CC vascularization including formation and proliferation of new blood
XX CC vessels, growth and development of tissues, tissue regeneration and organ
XX CC and tissue repair in a subject. The products of the invention are useful
XX CC for preparing medicaments for treating wounds such as dermal ulcers,
XX CC pressure sores, venous sores, diabetic ulcers and burns and to promote
XX CC skin graft growth, tissue repair, proliferation of new blood vessels,
XX CC tissue regeneration and organ repair by promoting angiogenic activity or
XX CC vascularization. This sequence represents a human VEGF-X protein
XX CC described in the method of the invention

XX Sequence 345 AA;

Query Match 99.6%; Score 1851; DB 3; Length 345;
Best Local Similarity 99.4%; Pred. No. 3.1e-178;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSFGLLLVTSALAGQRGTQAESNLSSKFOFSSNKQNGVQDPQHERIITVSTNGSIHS 60
Db 1 MSFGLLLVTSALAGQRGTQAESNLSSKFOFSSNKQNGVQDPQHERIITVSTNGSIHS 60
QY 61 PRFPHTYPRNTVLVRLVAVENYMIQLTFDERFGLDPEDDICKYDFVEVEEPSDGTIL 120
Db 61 PRFPHTYPRNTVLVRLVAVENYMIQLTFDERFGLDPEDDICKYDFVEVEEPSDGTIL 120
QY 121 GRWCGSGTVPCKQISKGNQIRIRFVSDEYFSPSESGFCIHYNIVMPQFTEAVSPVLPPSA 180
Db 121 GRWCGSGTVPCKQISKGNQIRIRFVSDEYFSPSESGFCIHYNIVMPQFTEAVSPVLPPSA 180
QY 181 LPDLNNNAITAFSTLEDLIRYLEPERWQLDLEDLYRFTWQLLGKAFVFGKSRVVDLNL 240
Db 181 LPDLNNNAITAFSTLEDLIRYLEPERWQLDLEDLYRFTWQLLGKAFVFGKSRVVDLNL 240
QY 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300
Db 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300
QY 301 VTKKYHEVLQRPKTGVRGLHKS LTDVALEHHEECDCVCRGSTGG 345
Db 301 VTKKYHEVLQRPKTGVRGLHKS LTDVALEHHEECDCVCRGSTGG 345

RESULT 14

AAB44322

ID AAB44322 standard; protein; 345 AA.

XX AC AAB44322;

XX DT 08-FEB-2001 (first entry)

XX XX Human PRO200 (UNQ174) protein sequence SEQ ID NO:488.

XX KW Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;
XX KW expressed sequence tag; detection; cancer.

XX OS Homo sapiens.

XX XX WO200053756-A2.

XX PN 14-SEP-2000.

XX PD 18-FEB-2000; 2000WO-US004341.

XX PF 08-MAR-1999; 99WO-US005028.

XX PR 12-MAR-1999; 99US-0123957P.

XX PR 29-MAR-1999; 99US-0126773P.

XX PR 21-APR-1999; 99US-0130232P.

XX PR 28-APR-1999; 99US-0131445P.

XX PR 14-MAY-1999; 99US-0134287P.

XX PR 23-JUN-1999; 99US-0141037P.

XX PR 26-JUL-1999; 99US-0145698P.

XX PR 30-OCT-1999; 99US-0162506P.

XX PR 30-NOV-1999; 99WO-US028313.

XX PR 02-DEC-1999; 99WO-US028551.

XX PR 16-DEC-1999; 99WO-US030095.

XX PR 30-DEC-1999; 99WO-US031243.

XX PR 30-DEC-1999; 99WO-US031274.

XX PR 05-JAN-2000; 2000WO-US000219.

XX PR 06-JAN-2000; 2000WO-US000277.

XX XX (GETH) GENENTECH INC.

XX PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;

PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX WPI: 2000-511443/58.
DR N-PSDB; AAC78582.

XX Novel PRO polypeptides and polynucleotides used in detection methods, to
PT target bioactive molecules to specific cells, and to modulate cellular
PT activities.

PS Claim 12; Fig 207; 636pp; English.

XX AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence
tag) sequences which encode secreted or transmembrane PRO polypeptides.
CC The PRO polynucleotides and polypeptides have cytotatic activity. The
CC polynucleotides and polypeptides can be used for detecting the presence
CC of PRO polypeptides in samples, for linking bioactive molecules to cells
CC and for modulating biological activities of cells, using the polypeptides
CC for specific targeting. The polypeptide targeting can be used to kill the
CC target cells, e.g. for the treatment of cancers. The polypeptide pairs
CC provide specific targeting of bioactive molecules to cells. AAC78600 to
CC AAC78987 represent PCR primers and probes used in the isolation of the
CC PRO polynucleotide sequences

XX Sequence 345 AA;

Query Match 99.6%; Score 1851; DB 3; Length 345;

Best Local Similarity 99.4%; Pred. No. 3.1e-178;

Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLFGLLLVTSALAGORRGTOAESNLSSKFQFSSNKEQNGVDPQHERIIIVSTNGSIHS 60

DB 1 MSLFGLLLVTSALAGORRGTOAESNLSSKFQFSSNKEQNGVDPQHERIIIVSTNGSIHS 60

QY 61 PRPHTYPRNTVLVRLVAIVENWVQLTDFRFGLEDPEDDICKYDFVEEPPSDGTIL 120

DB 61 PRPHTYPRNTVLVRLVAIVENWVQLTDFRFGLEDPEDDICKYDFVEEPPSDGTIL 120

QY 121 GRWCGSGTVPKGQISKGNQIRIRFVSDEYFSEPGFCIHYNVMPQFTEAVSPSLPPSA 180

DB 121 GRWCGSGTVPKGQISKGNQIRIRFVSDEYFSEPGFCIHYNVMPQFTEAVSPSLPPSA 180

QY 181 LPLDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWOLLGKAFVFGKSRVDNL 240

DB 181 LPLDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWOLLGKAFVFGKSRVDNL 240

QY 241 LTEEVRVLSCTPRNFSVSIRELKRDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300

DB 241 LTEEVRVLSCTPRNFSVSIRELKRDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300

QY 301 VTKKYHEVLQRPKTGVRLHKSLLTDVALEHHEECDCVCRGSTG 345

DB 301 VTKKYHEVLQRPKTGVRLHKSLLTDVALEHHEECDCVCRGSTG 345

RESULT 15

AAB24412
ID AAB24412 standard; protein; 345 AA.

XX AAB24412;

XX 07-NOV-2000 (first entry)

XX Human PRO713 protein sequence SEQ ID NO:137.

XX Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;
KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;
KW angiogenic; proliferative; cardiac; cardiovascular; antiatherosclerotic;
KW cytostatic; gene therapy; vaccine.
XX Homo sapiens.

XX WO200032221-A2.

XX 08-JUN-2000.

XX 30-NOV-1999; 99WO-US028313.

XX 01-DEC-1998; 98WO-US025108.

XX 16-DEC-1998; 98US-0112850P.

XX 12-JAN-1999; 99US-0115554P.

XX 08-MAR-1999; 99WO-US005028.

XX 12-MAR-1999; 99US-0123957P.

XX 28-APR-1999; 99US-0131445P.

XX 14-MAY-1999; 99US-0134287P.

XX 02-JUN-1999; 99WO-US012252.

XX 23-JUN-1999; 99US-0141037P.

XX 20-JUL-1999; 99US-0144758P.

XX 26-JUL-1999; 99US-0145698P.

XX 01-SEP-1999; 99WO-US020111.

XX 08-SEP-1999; 99WO-US020594.

XX 13-SEP-1999; 99WO-US020944.

XX 15-SEP-1999; 99WO-US021090.

XX 15-SEP-1999; 99WO-US021547.

XX 05-OCT-1999; 99WO-US023089.

XX 29-OCT-1999; 99US-0162506P.

XX (GETH) GENENTECH INC.

XX PA

XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ;

PI Goddard A, Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF;

PI Smith V, Watanabe CK, Williams PM, Wood WI;

XX WPI: 2000-412154/35.

XX N-PSDB; AAA77621.

XX Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing

PT and treating diagnosing a cardiovascular, endothelial or angiogenic

PT disorders in mammals.

XX Claim 72; Fig 50; 315pp; English.

XX The present invention describes nucleic acids encoding PRO polypeptides

CC useful for preventing, diagnosing and treating diagnosing a

CC cardiovascular, endothelial or angiogenic disorder in mammals by

CC modulating cell proliferation, angiogenesis and cardiovascularisation,

CC and for identifying agonists and antagonists of these processes. The

CC nucleic acids and the proteins they encode may be used in the prevention,

CC treatment and diagnosis of diseases associated with inappropriate PRO

CC expression such as cardiovascular, endothelial or angiogenic disorders in

CC mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For

CC example, the nucleic acids (NCs) and vectors containing them and the PRO

CC polypeptide may be used to treat disorders associated with decreased PRO

CC expression. AAA77510 to AAA77721 and AAB24388 to AAB24435 represent

CC nucleotide and protein sequences used in the exemplification of the

CC present invention

XX Sequence 345 AA;

Query Match 99.6%; Score 1851; DB 3; Length 345;

Best Local Similarity 99.4%; Pred. No. 3.1e-178;

Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLFGLLLVTSALAGORRGTOAESNLSSKFQFSSNKEQNGVDPQHERIIIVSTNGSIHS 60

DB 1 MSLFGLLLVTSALAGORRGTOAESNLSSKFQFSSNKEQNGVDPQHERIIIVSTNGSIHS 60

QY 61 PRPHTYPRNTVLVRLVAIVENWVQLTDFRFGLEDPEDDICKYDFVEEPPSDGTIL 120

DB 61 PRPHTYPRNTVLVRLVAIVENWVQLTDFRFGLEDPEDDICKYDFVEEPPSDGTIL 120

QY 121 GRWCGSGTVPKGQISKGNQIRIRFVSDEYFSEPGFCIHYNVMPQFTEAVSPSLPPSA 180

DB 121 GRWCGSGTVPKGQISKGNQIRIRFVSDEYFSEPGFCIHYNVMPQFTEAVSPSLPPSA 180

Qy	181	LPLDLLNNAITAFSTLEDLIIRYLEPERWOLDLEDLYRPTWOLLGKAFVFGKSRVVDLNL	240
Db	181	LPLDLLNNAITAFSTLEDLIIRYLEPERWOLDLEDLYRPTWOLLGKAFVFGKSRVVDLNL	240
Qy	241	LTEEVRLYSCTPRNFSVSIRBELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVP SK	300
Db	241	LTEEVRLYSCTPRNFSVSIRBELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVP SK	300
Qy	301	VTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHECDVCRCGSTGG	345
Db	301	VTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHECDVCRCGSTGG	345

Search completed: September 3, 2005, 19:25:47
Job time : 122.5 secs

Db 360 CDCIC 364

RESULT 2

JC7998

C:Species: Mus musculus (house mouse)

C:Date: 10-Nov-2003 #sequence_revision 10-Nov-2003 #text_change 24-Nov-2003

C:Accession: JC7998

R:Zhao, Y.; Hoyle, G.W.; Zhang, J.; Morris, G.; Lasky, J.A.

Biochem. Biophys. Res. Commun. 308, 126-132, 2003

A:Title: A novel murine PDGF-D splicing variant results in significant differences in platelet-derived growth factor-D - mouse

A:Reference number: JC7998; PMID:12890490

A:Accession: JC7998

A:Molecule type: mRNA

A:Residues: 1-370 <ZHU>

C:Comment: This protein is a potent mesenchymal cell mitogen and chemoattractant involved in platelet-derived growth factor-D - mouse

A:Gene: pdgf-D

A:Introns: 42/2; 110/1; 170/2; 191/2; 258/2; 330/1; 334/2

C:Keywords: fibrosis; PDGF-D

Query Match 39.7%; Score 737.5; DB 2; Length 370;

Best Local Similarity 44.0%; Pred. No. 1.5e-55;

Matches 153; Conservative 59; Mismatches 103; Indels 33; Gaps 9;

QY 16 QRRGQAESNLSKQFQSNKEQGVQD-PQHERITVTSGSIHSPRPHTYPRNTVLV 74

Db 26 QRASIKALRNANLR-----RDESNHLTDLQYRENIQVTSNGHVQSPRPNSYPRNLLLT 80

QY 75 WRLVAEENVMTQLTDFRFGLEDDEDDICKYDFVEVEEPSDGT--ILGRWCGSGTVP GK 132

Db 81 WMLRS-QBKTRIQLSQDFQGLEAENDICRYDFVEVESESVTVVRGRCWGHKEIPPR 139

QY 133 QISKGNQIRIRFVSDYFPPSEPGFCIHYNVMPQTEAV-----SPS 174

Db 140 ITSRTNQIKITPKSDDYFAKEGFKIYSFVEDFQPEASETNWESVTSFSGVSYHSPS 199

QY 175 VLPPALPLDLNNAITAFSTLEDLIRYLEPBERWOLDLEDLIRPFWQLLKGAFVGRKSR 234

Db 200 ITDPT-LTADALDKTVASFDTVEDLLKHFNVPVSWQDDLENLYDTPHYRGRSY-HDRKSK 257

QY 235 VVDNLNLTVEVRLYCTRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLNHCNEC 294

Db 258 -VDLRLNDDVKRYSCTRFNHSVNLEKELTNVAFPRCLLVQRCCGCGGTWNWKCSC 316

QY 295 QCVPKSKTKKXHEVLQLRP---KTGVRGLHKS LTDVALEHHEECDCVC 339

Db 317 TCSSGKTKVKYHEVLKFPFGHFKRGGKAKNMALVDIQLDHERCDCIC 364

RESULT 3

JC7592

C:Species: Rattus norvegicus (Norway rat)

C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004

C:Accession: JC7592

R:Hamada, T.; Uti-Tel, K.; Imaki, J.; Miyata, Y.

Biochem. Biophys. Res. Commun. 280, 733-737, 2001

A:Title: Molecular cloning of SCDFG-B, a novel growth factor homologous to SCDFG-C/

A:Reference number: JC7591; PMID:21092670; PMID:11162582

A:Contents: Fetal brain

A:Accession: JC7592

A:Molecule type: mRNA

A:Residues: 1-370 <HAM>

A:Cross-references: UNIPROT:Q9EQT1; DDBJ:AB052170

C:Genetics:

A:Gene: scdfg-B

F:1-17/Domain: secretory signal sequence #status predicted <SIG>

F:18-370/Product: spinal cord-derived growth factor-B #status predicted <MAT>

F:52-170/Region: CUB domain #status predicted

F:272-370/Region: homologous to platelet-derived growth factor/vascular endothelial growth factor

F:294-308/Region: conserved motif #status predicted

Query Match 39.6%; Score 736; DB 2; Length 370;

Best Local Similarity 45.6%; Pred. No. 2.1e-55;

Matches 149; Conservative 57; Mismatches 93; Indels 28; Gaps 9;

QY 37 BONGVQD-PQHERITVTSGSIHSPRPHTYPRNTVLVWRLVAEENVMTQLTDFRFG 95

Db 42 ESNHLTDLRYDENIRVTGTHVQSPRPNSYPRNLLTWRLHS-QEKTRIQLAFDHQFG 100

QY 96 LEDPEDDICKYDFVEVEEPSDGT--ILGRWCGSGTVPFGKQISKGNQIRIRFVSEYFPE 153

Db 101 LEEAENDICRYDFVEVEDSVSSVVRGRCWGHKEIPRITSRTNQIKITFQSDDYFAK 160

QY 154 PGFCIHYNIV--MPQTEAV-----SPSVLPSPALPLDLNNAITAFST 195

Db 161 PGFKIYYSFVDFQPEASEINWESVTSFSGVSYHSPSVN-DSTLTADALDKAIEPDT 219

QY 196 LEDLIRYLEPBERWOLDLEDLIRPFWQLLKGAFVGRKSRVVDLNLNLTVEVRLYCTPRNF 255

Db 220 VEDLLKYNFASWQDDLENLYDTPHYRGRSY-HERKSK-VDLRLNDDVKRYSCTRNH 277

QY 256 SVSIREELKRTDTIFWPGCLLVKRCGNCACCLNHCNECQCVPSKVTKYKXHEVLQLRP-- 313

Db 278 SVNLREELKLTNAVFFPRCLLVQRCCGCGGTLNWKSCTCSGKTKVKYHEVLKFPBGH 337

QY 314 -KTGVRGLHKS LTDVALEHHEECDCVC 339

Db 338 FRRGKAKNMALVDIQLDHERCDCIC 364

RESULT 4

T09456

Intrinsic factor-B12 receptor Cubilin precursor - human

C:Species: Homo sapiens (man)

C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004

C:Accession: T09456

R:Kozyraki, R.; Kristiansen, M.; Silahatoglu, A.; Hansen, C.; Tommerup, N

Blood 99, 3593-3600, 1998

A:Title: The human intrinsic factor-vitamin B12 receptor, cubilin: Molecular characterization.

A:Reference number: Z16677; MUID:98241400; PMID:9572993

A:Accession: T09456

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-3623 <KOZ>

A:Cross-references: UNIPROT:O60494; EMBL:AF034611; NID:G3292528; PIDN:AAC82612.1; PID:G9

C:Genetics:

A:Map position: 10p12

C:Superfamily: intrinsic factor-B12 receptor cubilin; EGF homology

C:Keywords: receptor; vitamin B12 uptake

F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-3623/Product: intrinsic factor-B12 receptor #status predicted <MAT>

F:436-467/Domain: EGF homology <EGF>

Query Match 9.8%; Score 183; DB 2; Length 3623;

Best Local Similarity 26.2%; Pred. No. 1.1e-06;

Matches 96; Conservative 42; Mismatches 139; Indels 90; Gaps 23;

QY 19 QTOAESNLSSKQFQ-----SSNKEQNG-----VQDPQHERITVTSGSIHSPRPFH 65

Db 892 GTDIPSFITSYVNFYLVTFVKSSSTENHGFMAKFAEDLACGEILTEST-GTIQSPGHFN 950

QY 66 TYPRNTVLVWRLVAEENVMTQLTDFRFGLEDDEDDICKYDFVEVEEPSDGTILGRWG 125

Db 951 VYPHGINCTWHIL-VQPNHLIHLMF-ETFHLEFHYN--CTNDYLEVDYDTSLSGRVCG 1006

QY 126 SGTVPGKQISKGNQIRIRFVSDYFPPSPGFCIHYNIV-----MPQTEAVSPSVLPPS 179

Db 1007 K-STPPSLTSSGSLMLVFVTDSDLAYE-GFLINYEALSAATACLDYTDGLTFTSP-- 1062

QY 180 ALPLDLNNAITAFSTLEDLIRYLEPBERWOLDLEDLIRPFWQLLKGAFVGRKSRV 236

Db 1063 ----NFPNN-----YPNW-----ECIVRITVTRTGIIAVHFTNFSLEAI 1099

A;Accession: JH0466
A;Molecule type: mRNA
A;Residues: 1-927 <FAK>
A;Cross-references: GB:D10467; GB:D01077; NID:G222962; PIDN:BAAO1260.1; PID:G222963
A;Experimental source: tadpole, brain
A;Note: this protein has motifs homologous to complement components C1r and C1s and to C3
C;Comment: This protein is a neuronal cell surface molecule involved in the neuronal rec
C;Superfamily: Xenopus A5 antigen; C1r/C1s repeat homology; discoidin I amino-terminal h
C;Keywords: duplication; glycoprotein; transmembrane protein

	Query Match	9.7%;	Score 179.5;	DB 1;	Length 927;	
	Best Local Similarity	31.6%;	Pred. No. 4.1e-07;			
	Matches 55; Conservative	29;	Mismatches 73;	Indels 17;	Gaps 7;	
Qy	50	ITVSTNGSHTSPRFPHTYPRNTVLVMRLVAVENYWIQLTFDEREGLEDPEDDICKYDFV	109			
	:	:::	: :: :	:	:: :	:
	:	:	:	:	:	:
Db	31	IKITSPYSITSAGYPHSPYPPSORCWLQIAPPHYQRIMFNPHFDLEDR---	CKYDIV 87			
	:	:	:	:	:	:
Qy	110	EV--EPPSDGTLILRCWCGSGTVPGKQISKGNQIRIRFVSDEYFPFSEPGFCIHYNLMP---	165			
	:	:	:	:	:	:
Db	88	EVIDGDNANGOLLGYKCYGR-IAPSLAVSTGPSIFIRFVSVDYETPG-AGEFSIREVEFKTGP	145			
	:	:	:	:	:	:

N: Alternate names: bone morphogenic protein 1
C: Species: Xenopus laevis (African clawed frog)
C: Date: 30-Sep-1993
C: Accession: J03218
R: Maeno, M.; Xue, Y.; Wood, T.I.; Ong, R.C.; Kung, H.
Gene 134, 257-261, 1993
A: Title: Cloning and expression of cDNA encoding Xenopus laevis bone morphogenetic protein 1
A: Reference number: J03218; PMID:94085787; PMID:82623184
#text_change 09-Jul-2004

A;Title: Cloning and expression of cDNA encoding xenopus laevis bone morphogenetic protein 10
A;Reference number: JC2218; MUID:94085787; PMID:8262384

C; Superfamily: procollagen C-endopeptidase; astacin homology; C1r/C1s repeat homology; E
C; Keywords: beta-hydroxyasparagine; glycoprotein; hydrolase; metalloproteinase; zinc
F; 93-284/Domain: astacin homology <AST>

F:398-510/Region: complement 11/18-like repeat
F:398-507/Domain: C1r/C1s repeat homology <C1R2>

Query Match 9.5%; Score 176; DB 2; Length 707;
Best Local Similarity 43.3%; Pred. No. 5.9e-07;
F:52/105,295,325/Binding site: carboxyrate (Asn) (covalent) #status predicted
F:176,180,186,235/Binding site: zinc (His, His, Tyr) #status predicted
F:177/Active site: Glu #status predicted
F:528/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match 9.5%; Score 176; DB 2; Length 707;
Best Local Similarity 43.3%; Pred. No. 5.9e-07;

J. Biol. Chem. 269, 32572-32578, 1994
A:Title: Bone morphogenetic protein-1 and a mammalian tolloid homologue (mTld) are encoded by two genes in the mouse genome
A:Reference number: A58788; MUID:95096114; PMID:7798260
A:Accession: B58788
A:Molecule type: mRNA
A:Residues: 703-986 <TA>
A:Cross-references: GB:L35279; NID:9619860; PIDN:AA41710.1; PID:9619861
C:Genetics:
A:Gene: GDB:BMP1; BMP-1
A:Cross-references: GDB:125203; OMIM:112264
A:Map position: 8p21-8p21
C:Function:
A:Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen type I procollagen
C:Superfamily: procollagen C-endopeptidase; astacin homology; C1r/C1s repeat homology; EGF homology
C:Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; gl
F:1-22/Domain: signal sequence #status predicted <SIG>
F:123-986/Product: procollagen C-endopeptidase tolloid-like splice form #status predicted
F:130-321/Domain: astacin homology <AST>
F:132-431/Domain: C1r/C1s repeat homology <C1R1>
F:135-544/Domain: C1r/C1s repeat homology <C1R2>
F:435-587/Domain: EGF homology <EG1>
F:591-700/Domain: C1r/C1s repeat homology <C1R3>
F:707-742/Domain: EGF homology <EG2>
F:747-856/Domain: C1r/C1s repeat homology <C1R4>
F:860-973/Domain: C1r/C1s repeat homology <C1R5>
F:911-142/332,363,599/Binding site: carboxylate (Asn) (covalent) #status predicted
F:163-319,185-205,322-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,644-666/Modified site: zinc (His, His, His, Tyr) #status predicted
F:213,217,223,272/Binding site: zinc (His, His, His, Tyr) #status predicted
F:214/Active site: Glu #status predicted
F:565,720/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
Query Match 9.1%; Score 169; DB 1; Length 986;
Best Local Similarity 39.4%; Pred. No. 3.6e-06;
Matches 43; Conservative 17; Mismatches 39; Indels 10; Gaps 5;
QY 55 NGSIHSPRPHTYPRNTVLVWRLVA-VEENVMIQTLTDFRFGLEDPEDDICKYDFVEVE 113
DB 599 NGSITSPGPKPEYPPKNCINQVLVAPTQYRISLQDFETEG-----NDVCKYDFVEVRS 653
QY 114 --PSDGTILGRCGSGTVPKGQISKGNOIRIRFVSDYFPSPGFCIH 160
DB 654 GLTADSKLHGKFCGS-EKPEVITSQYNNMRVFEKSDNTV-SKKGFKAHP 700
RESULT 11
I49540
procollagen C-endopeptidase (EC 3.4.24.19) precursor, tolloid-like splice form - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I49540
R:Fukagawa, M.; Noboru, S.; Hogan, B.L.M.; Jones, C.M.
Dev. Biol. 163, 175-183, 1994
A:Title: Embryonic expression of mouse bone morphogenetic protein-1 (BMP-1) which is related to the human bone morphogenetic protein-1 (BMP-1) which is related to human bone
A:Reference number: I49540; MUID:94229342; PMID:8174772
A:Accession: I49540
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-991 <RES>
A:Cross-references: UNIPROT:P98063; GB:L24755; NID:9439606; PIDN:AAA37306.1; PID:9439607
C:Genetics:
A:Gene: Bmp-1
C:Superfamily: procollagen C-endopeptidase; astacin homology; C1r/C1s repeat homology; EGF homology
F:135-326/Domain: astacin homology <AST>
F:556-592/Domain: EGF homology <EG1>
F:596-705/Domain: C1r/C1s repeat homology <C1R>
F:712-747/Domain: EGF homology <EG2>
F:218,222,228,277/Binding site: zinc (His, His, His, Tyr) #status predicted
F:219/Active site: Glu #status predicted
Query Match 9.1%; Score 169; DB 2; Length 991;
Best Local Similarity 39.4%; Pred. No. 3.6e-06;
Matches 43; Conservative 17; Mismatches 39; Indels 10; Gaps 5;

QY 55 NGSIHSPRPHTYPRNTVLVWRLVA-VEENVMIQTLTDFRFGLEDPEDDICKYDFVEVE 113
DB 604 NGSITSPGPKPEYPPKNCINQVLVAPTQYRISLQDFETEG-----NDVCKYDFVEVRS 658
QY 114 --PSDGTILGRCGSGTVPKGQISKGNOIRIRFVSDYFPSPGFCIH 160
DB 659 GLTADSKLHGKFCGS-EKPEVITSQYNNMRVFEKSDNTV-SKKGFKAHP 705
RESULT 12
A5362
procollagen I C-proteinase enhancer protein precursor - human
C:Species: Homo sapiens (man)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 15-Mar-2004
C:Accession: A5362
R:Takahara, K.; Kessler, E.; Biniaminov, L.; Brusel, M.; Eddy, R.L.; Jani-Sait, S.; Show J. Biol. Chem. 269, 26280-26285, 1994
A:Title: Type I procollagen COOH-terminal proteinase enhancer protein: identification, p
A:Reference number: A5362; MUID:95014462; PMID:7523404
A:Accession: A5362
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-449 <TA>
A:Cross-references: GB:L33799; NID:9642907; PIDN:AAA61949.1; PID:9642908
C:Genetics:
A:Gene: GDB:PCOLCE
A:Cross-references: GDB:305468; OMIM:600270
A:Map position: 7q21.3-7q22
C:Keywords: extracellular protein; glycoprotein; pyroglutamic acid
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-449/Product: #status predicted <MAT>
F:37-146/Domain: C1r/C1s repeat homology <C1R1>
F:159-270/Domain: C1r/C1s repeat homology <C1R2>
F:26/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F:29,431/Binding site: carboxylate (Asn) (covalent) #status predicted
Query Match 8.3%; Score 154; DB 2; Length 449;
Best Local Similarity 33.8%; Pred. No. 2.6e-05;
Matches 48; Conservative 22; Mismatches 50; Indels 22; Gaps 10;
QY 56 GSIHSPRPHTYPRNTVLVWRLVA-VEENVMIQTLTDFRFGLEDPEDDICKYDFVEV--- 111
DB 168 GLTTPNWPESDYPGSGSCWHIIAPPDQV-IALTFF-EKFDLE--PDYCRYDSVSFENG 223
QY 112 EEPDGTILGRCGSGTVPKGQISKGNOIRIRFVSDYFPSPGFCIH 168
DB 224 AVSDSRRLGKFCGD-AVPGSISSEGNELLYQFVSDLSVTAD-GFSASYK-TLPRGTAK 280
QY 169 -----EAVSPSV-LPPSALP 182
DB 281 QGGPGPKRGTEPKVKLPKPSQP 302
RESULT 13
A39288
dorsal-ventral patterning protein tolloid (EC 3.4.24.-) - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A39288
R:Shimell, M.J.; Ferguson, E.L.; Childs, S.R.; O'Connor, M.B.
Cell 67, 469-481, 1991
A:Title: The Drosophila dorsal-ventral patterning gene tolloid is related to human bone morphogenetic protein-1 (BMP-1) which is related to human bone
A:Reference number: A39288; MUID:92034970; PMID:1840509
A:Accession: A39288
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1057 <SHI>
A:Cross-references: UNIPROT:P25723; GB:M76976; NID:9157305; PIDN:AAA28491.1; PID:9157306
C:Genetics:
A:Gene: FlyBase:tlid
A:Cross-references: FlyBase:FBgn0003719
C:Superfamily: dorsal-ventral patterning protein tolloid; astacin homology; C1r/C1s repeat

C;Keywords: duplication; hydrolase; metalloproteinase; zinc
F:136-329/Domain: astacin homology <AST>
F:352-464/Domain: C1r/C1s repeat homology <C1r1>
F:468-578/Domain: C1r/C1s repeat homology <C1r2>
F:585-620/Domain: EGF homology <EG1>
F:624-740/Domain: C1r/C1s repeat homology <C1r3>
F:747-782/Domain: EGF homology <EG2>
F:787-896/Domain: C1r/C1s repeat homology <C1r4>
F:900-1013/Domain: C1r/C1s repeat homology <C1r5>
F:1221,225,231,280/Binding site: zinc (His, His, His, Tyr) #status predicted
F:222/Active site: Glu #status predicted

Query Match 8.0%; Score 148.5; DB 1; Length 1057;
Best Local Similarity 38.0%; Pred. No. 0.00022;
Matches 38; Conservative 20; Mismatches 35; Indels 7; Gaps 5;
QY 50 ITVSTNGSIHSPPRFTYPRNTVLVRLVAEENVMWQLTFDERFGLDEPDDICKYDFV 109
DB 472 LKLTQDSIDSPNYPMDYMPDKECVWRITA-PDNHVALKF-QSFELE--KHDGCAYDFV 527
QY 110 EVEE--PSDGTILGRWCGSGTVPGKQISGNQIRIRFVSD 147
DB 528 EIRNGNHSRLIGRFGCDKLPNLIK-TRSNQMYIRFVSD 566

RESULT 14
A:Accession: A59271
RA-reactive factor (EC 3.4.21.-) 2 precursor - human
N:Alternate names: mannose binding protein-associated serine proteinase 2 (MASP-2)
C:Species: Homo sapiens (man)
C:Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C:Accession: A59271
R:Rifael, S.; Vorup-Jensen, T.; Stover, C.M.; Schwaebler, W.J.; Laursen, S.B.; Poulsen, K.
Nature 386, 506-510, 1997
A:Title: A second serine protease associated with mannan-binding lectin that activates complement
A:Reference number: A59271; MUID:97242412; PMID:9087411
A:Accession: A59271
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-686 <JEN>
A:Cross-references: UNIPROT:O00187; GB:Y09926; NID:G4007626; PIDN:CAA71059.1; PID:G40076
A:Experimental source: tissue liver
A:Note: submitted to GenBank, December 1996
A:Note: parts of this sequence, including the amino end of the mature protein, were determined
C:Genetic: GDB:MASP2
A:Gene: GDB:MASP2
A:Cross-references: GDB:6071500
A:Map position: lp36.2-lp36.3
C:Superfamily: complement-activating serine proteases C1r/C1s/MASP; C1r/C1s repeat homology
C:Keywords: beta-hydroxyasparagine; complement pathway; duplication; hydrolase; serine protease
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-444,445-686/Product: Ra-reactive factor 2 #status predicted <MAT>
F:19-134/Domain: C1r/C1s repeat homology <C1r1>
F:142-180/Domain: EGF homology <EGF>
F:184-293/Domain: C1r/C1s repeat homology <C1r2>
F:300-361/Domain: complement factor H repeat homology <EH1>
F:366-430/Domain: complement factor H repeat homology <EH2>
F:445-679/Domain: trypsin homology <TRY>
F:72-90,142-156,167-180,184-211,241-259,300-348,328-361,366-412,396-430,434-552,
F:158/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
F:444-445/Cleavage site: Arg-Ile (autolytic) #status predicted
F:483,532,633/Active site: His, Asp, Ser #status predicted

Query Match 7.7%; Score 143.5; DB 1; Length 686;
Best Local Similarity 32.1%; Pred. No. 0.00035;
Matches 34; Conservative 25; Mismatches 42; Indels 5; Gaps 4;
QY 55 NGSISPPRFTYPRNTVLVRLVAEENVMWQLTFDERFGLDEPDDICKYDFVEVEP 114
DB 193 SGELSSPPRFPYKLSCTYS-ISLEGFSVILDFVESFDVETHELCPYDFLKIQ-- 249
QY 115 SDGTTILGRWCGSGTVPGKQISGNQIRIRFVSDVPPSPFGFCIH 160

DB 250 TDBEHGPFCKG-TLPHRIETKSNVTITTFVTDE-SGDHTGKWIHY 293

RESULT 15

T31069
tolloid-BMP-1 like protein 1 - California sea hare
N:Alternate names: probable metalloprotease TBL-1
C:Species: Aplysia californica (California sea hare)
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C:Accession: T31069
R:Li, Q.R.; Hattar, S.; Endo, S.; MacPhee, K.; Zhang, H.; Cleary, J.H.; Byrne, L.J.; Byrne, J.H.; Es-
J. Neurosci. 17, 755-764, 1997
A:Title: A developmental gene (Tolloid/BMP-1) is regulated in Aplysia Neurons by treatment
A:Reference number: Z20965; MUID:98007484; PMID:8987797
A:Accession: T31069
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1070 <LIU>
A:Cross-references: UNIPROT:P91972; EMBL:U57369; NID:G1899041; PID:G1899042; PIDN:AA474
C:Superfamily: dorsal-ventral patterning protein tolloid; astacin homology; C1r/C1s repeat

Query Match 7.5%; Score 139.5; DB 2; Length 1070;
Best Local Similarity 21.9%; Pred. No. 0.0013;
Matches 70; Conservative 36; Mismatches 102; Indels 111; Gaps 17;
QY 56 GSIHSPPRFTYPRNTVLVRLVAEENVMWQL--TFDERFGLDEPDDICKYDFVEVE 112
DB 529 GFLNSPAYPDYGDQKVCWM-VITVREGYQVAFETAFETEF--DPD--CAYDYVEIR 581
QY 113 --EPDGTILGRWCGSGTVPGKQISGNQIRIRFVSDYFPSPFGFCIH 160
DB 592 DGDTKDSPLVGTCGTRT-PNNAISTSRHLVVKFVSDSM-QKGGFSASYLEEVDCEGE 639
QY 161 -----NIVMPQFTEAVSPSV 175
DB 640 DHGCHVCVNTLGSVECTCKIGYELHSDGKCEKACGGYLDAPSGTISSPSF-----PD 694
QY 176 LPPSALPDLNNAITAFS-----TLEDLIRYLPERWQLDLDLYRPTWLLGKAFVG 230
DB 695 YPPD-----KNCVWHISAPKGHILTIVNFTMDLE-WRGDECEL-----DFVRVTNVVG 741
QY 231 RKSRRVDLNLLEEVRLYSCTPRNFSVS--IREELKRTDTTFWPGCLL-----VKRCG 283
DB 742 NKER-----LQGGYCGGMAPPSITSLSNELRIEPRSDTLQKTGFSMDYADVDECCASS 795
QY 284 CACLLHNCN-----ECOC 296
DB 796 NGGCKHICENTVGSFHCSC 814

Search completed: September 3, 2005, 19:30:37
Job time : 27.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 3, 2005, 19:09:34 ; Search time 114.5 Seconds
(without alignments)
1542.946 Million cell updates/sec

Title: US-09-818-943-1
Perfect score: 1858
Sequence: 1 MSLFGLLLVTSALAGQRRGT.....DVALEHHBECDCVCRGSTGG 345

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1858	100.0	345	2 Q9NRA1	Q9nra1 homo sapien
2	1851	99.6	345	2 Q9UL22	Q9ul22 homo sapien
3	1664	89.6	345	2 Q9QY71	Q9qy71 m fallotein
4	1662	89.5	345	2 Q8CI19	Q8ci19 mus musculu
5	1646	88.6	345	2 Q9QXK6	Q9eqx6 rattus norv
6	1635	88.0	345	2 Q9JHV8	Q9jnv8 mus musculu
7	1614	86.9	345	2 Q91946	Q91946 gallus gall
8	1260	67.8	258	2 Q8K429	Q8k429 rattus norv
9	741.5	39.9	370	2 Q9GZP0	Q9gzp0 homo sapien
10	740.5	39.9	364	2 Q9BWV5	Q9bwv5 homo sapien
11	737.5	39.7	370	2 Q9Z5I7	Q9z5i7 mus musculu
12	736	39.6	370	2 Q9EQT1	Q9eqt1 rattus norv
13	669.5	36.0	300	2 Q6V9H4	Q6v9h4 oryctolagus
14	435.5	23.4	261	2 Q8K2L3	Q8k2l3 mus musculu
15	190.5	10.3	923	1 NR1P_BRARE	Q8qfx6 brachydanio
16	190.5	10.3	923	2 Q69D88	Q69db8 brachydanio
17	183	9.8	3494	2 Q71C53	Q71c53 homo sapien
18	183	9.8	3623	2 Q60494	Q60494 homo sapien
19	182	9.8	691	2 Q57658	Q57658 gallus gall
20	181.5	9.8	871	2 Q67869	Q6t869 brachydanio
21	181.5	9.8	959	2 Q69DB7	Q69db7 brachydanio
22	181.5	9.8	959	2 Q6RT22	Q6rt22 brachydanio
23	181.5	9.8	959	2 Q6T870	Q6t870 mus musculu
24	180	9.7	34	2 Q9JUM4	Q9jtm4 mus musculu
25	179.5	9.7	928	1 NR1P_XENLA	P28824 xenopus lae
26	176	9.5	707	1 BNP1_XENLA	P98070 xenopus lae
27	176	9.5	977	2 Q91925	Q91925 xenopus lae
28	176	9.5	3623	2 Q70244	Q70244 rattus norv
29	173.5	9.3	616	1 SPAN_STRPU	P98068 strongyloce
30	172	9.3	1012	2 Q9WVM6	Q9wvm6 mus musculu
31	171	9.2	735	2 Q57381	Q57381 xenopus lae

32	171	9.2	735	2	Q66K13	Q66ki3	xenopus lae
33	171	9.2	1015	2	Q9Y6L7	Q9y6l7	homo sapien
34	171	9.2	1078	2	Q9UQ00	Q9uq00	homo sapien
35	169	9.1	241	2	Q9Z135	Q9z135	rattus norv
36	169	9.1	775	2	Q6P550	Q6p550	mus musculus
37	169	9.1	986	1	BNP1_HUMAN	P13497	homo sapien
38	169	9.1	991	1	BNP1_MOUSE	P98063	mus musculus
39	169	9.1	991	2	Q6NZM2	Q6nzm2	mus musculus
40	165.5	8.9	145	2	Q8BP20	Q8bp20	mus musculus
41	165.5	8.9	926	2	Q8QZV7	Q8qzv7	mus musculus
42	164.5	8.9	555	2	Q9H2E2	Q9h2e2	homo sapien
43	164.5	8.9	901	2	Q9H2D5	Q9h2d5	homo sapien
44	164.5	8.9	901	2	Q9H2E4	Q9h2e4	homo sapien
45	164.5	8.9	906	2	Q9H2D4	Q9h2d4	homo sapien

ALIGNMENTS

RESULT 1
Q9NRA1
ID Q9NRA1 PRELIMINARY; PRT; 345 AA.
AC Q9NRA1;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Platelet-derived growth factor C.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=20268201; PubMed=10806482; DOI=10.1038/35010579;
RA Li X., Ponten A., Aase K., Karlsson L., Abramson A., Uutela M.,
RA Backstrom G., Hellstrom M., Bostrom H., Li H., Soriano P.,
RA Betsholtz C., Heldin C.-H., Alitalo K., Ostman A., Eriksson U.;
RT "PDGF-C is a new protease-activated ligand for the PDGF alpha-
RT receptor.";
RL Nat. Cell Biol. 2:302-309(2000)
CC -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
DR EMBL; AF244813; AAF80597.1; -.
DR HSSP; Q9JJS8; 1NT0.
DR Genew; HGNC:8801; PDGFC.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008283; P:cell proliferation; IEA.
DR GO; GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00341; PDGF; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS02078; PDGF_2; 1.
KW Growth factor; Mitogen.
SQ SEQUENCE 345 AA; 39043 MW; 590889CEA55CC5EA CRC64;

Query Match 100.0%; Score 1858; DB 2; Length 345;
Best Local Similarity 100.0%; Pred. No. 3.1e-150;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSLFGLLLVTSALAGQRRGTQAESNLSSKQFSSNKEQNGVQDPQHERIIIVSTNGSIHS 60
DB 1 MSLFGLLLVTSALAGQRRGTQAESNLSSKQFSSNKEQNGVQDPQHERIIIVSTNGSIHS 60
QY 61 PRFPHYTNTLVVRLVAEENWVIOQTDFRFGLEDPEDDICKYDFVEEPEPSDGTIL 120
DB 61 PRFPHYTNTLVVRLVAEENWVIOQTDFRFGLEDPEDDICKYDFVEEPEPSDGTIL 120
QY 121 GRWCGSVTPGKQISKGNQIRIRFVSDYFFSEFGFCHYINIVMPQFTEAVSPSLPPSA 180

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Db 121 GRWCSGTVPKQISKGNQIRIRFVSDEYFSPERGFCIHYNIVMPQFTEAVSPSVLPSPA 180
QY 181 LPDLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLKGAFVFGKRSRVVDLNL 240
Db 181 LPDLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLKGAFVFGKRSRVVDLNL 240
QY 241 LTEEVRVLSCTPRNFSVSIRELKTDTTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300
Db 241 LTEEVRVLSCTPRNFSVSIRELKTDTTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300
QY 301 VTKKYHEVLQRPKTVGRGLHSLTDVALEHHEEDCDVCRGSTGG 345
Db 301 VTKKYHEVLQRPKTVGRGLHSLTDVALEHHEEDCDVCRGSTGG 345

RESULT 2
Q9UL22 PRELIMINARY; PRT; 345 AA.
AC Q9UL22;
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 05-JUL-2004 (TremBLrel. 27, Last annotation update)
DE Secretory growth factor-like protein fallotain (Spinal cord-derived growth factor) (Platelet-derived growth factor C) (VEGF-E).
GN Name=hSCDGF; Synonyms=PDGFC; ORFNames=UNQ174;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RX MEDLINE=20461776; PubMed=11004490; DOI=10.1016/S0167-4781(00)00066-X;
RA Tsai Y.-J., Lee R.K., Lin S.-P., Chen Y.-H.;
RT "Identification of a novel platelet-derived growth factor-like gene, fallotain, in the human reproductive tract.";
RL Biochim. Biophys. Acta 1492:196-202(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=20317014; PubMed=10858496; DOI=10.1016/S0014-5793(00)01640-9;
RA Hamada T., Ui-Tei K., Miyata Y.;
RT "A novel gene derived from developing spinal cords, SCDGF, is a unique member of the PDGF/VEGF family.";
RL FEBS Lett. 475:97-102(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21347863; PubMed=11297552; DOI=10.1074/jbc.M101056200;
RA Gilbertson D.G., Duff M.E., West J.W., Kelly J.D., Sheppard P.O., Hofstrand P.D., Gao Z., Shoemaker K., Bukowski T.R., Moore M., Feldhaus A.L., Humes J.M., Palmer T.E., Hart C.B.;
RT "Platelet-derived growth factor C (PDGF-C), a novel growth factor that binds to PDGF alpha and beta receptor.";
RL J. Biol. Chem. 276:27406-27414(2001).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Eaton J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R., Watanabe C., Wiedand D., Woods K., Xie M.H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I., Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AF091434; AAF00049.1; -.
DR EMBL; AB033831; BAB03266.1; -.

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DR EMBL; AF260738; AAK51637.1; -.
DR EMBL; AY358493; AAO88857.1; -.
DR HSP; Q9JUS8; INTO.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0008083; F:growth factor activity; TAS.
DR GO; GO:0007417; P:central nervous system development; TAS.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00341; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS50278; PDGF 2; 1.
DR SEQUENCE 345 AA; 39029 MW; CDB9E51F40633E78 CRC64;

Query Match 99.6%; Score 1851; DB 2; Length 345;
Best Local Similarity 99.4%; Pred. No. 1.2e-149;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLFGLLLVTSALAGORRGTOAESNLSSKQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60
Db 1 MSLFGLLLVTSALAGORRGTOAESNLSSKQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60
QY 61 PRPHITYPRNTVLVRLVAVENVMWQLTDFERFGLDEPDDICKYDFVVEEPPSDGITL 120
Db 61 PRPHITYPRNTVLVRLVAVENVMWQLTDFERFGLDEPDDICKYDFVVEEPPSDGITL 120
QY 121 GRWCSGTVPKQISKGNQIRIRFVSDEYFSPERGFCIHYNIVMPQFTEAVSPSVLPSPA 180
Db 121 GRWCSGTVPKQISKGNQIRIRFVSDEYFSPERGFCIHYNIVMPQFTEAVSPSVLPSPA 180
QY 181 LPDLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLKGAFVFGKRSRVVDLNL 240
Db 181 LPDLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLKGAFVFGKRSRVVDLNL 240
QY 241 LTEEVRVLSCTPRNFSVSIRELKTDTTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300
Db 241 LTEEVRVLSCTPRNFSVSIRELKTDTTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300
QY 301 VTKKYHEVLQRPKTVGRGLHSLTDVALEHHEEDCDVCRGSTGG 345
Db 301 VTKKYHEVLQRPKTVGRGLHSLTDVALEHHEEDCDVCRGSTGG 345

RESULT 3
Q9Y71 PRELIMINARY; PRT; 345 AA.
AC Q9Y71;
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
DT 25-OCT-2004 (TremBLrel. 28, Last annotation update)
DE Fallotin (Platelet-derived growth factor C) (Mus musculus adult male cecum cDNA, RIKEN full-length enriched library, clone:9130403008 DE product:platelet-derived growth factor, C polypeptide, full insert DE sequence) (Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730022G11 product:platelet-derived DE growth factor, C polypeptide, full insert sequence) (Mus musculus 15 days embryo head cDNA, RIKEN full-length enriched library, DE clone:D93000LM08 product:platelet-derived growth factor, C DE polypeptide, full insert sequence).
GN Name=PDGfc;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA Tsai Y.-J., Lee R.K.-K., Chen Y.-H., Lin S.-P., Cheng W.T.-K.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Gao Z., Hart C., Piddington C., Sheppard P., Shoemaker K.,

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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalios D.E., Schmerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Mammary tumor;
RA Strassberg R.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
DR EMBL; BC037696; AAH37696.1; -.
DR HSSP; Q9JUS8; LNT0.
DR MGD; MGI:1859631; Pdgfc.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0005161; P:platelet-derived growth factor receptor bin. .; IDA.
DR GO; GO:0008284; P:positive regulation of cell proliferation; IDA.
DR GO; GO:0050730; P:regulation of peptidyl-tyrosine phosphoryla. .; IDA.
DR GO; GO:0007171; P:transmembrane receptor protein tyrosine kin. .; IDA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00341; PDGF; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF_2; 1.
DR Growth factor; Mitogen.
SQ SEQUENCE 345 AA; 38741 MW; 9A58A05C6C0E9614 CRC64;

Query Match 89.5%; Score 1662; DB 2; Length 345;
Best Local Similarity 86.4%; Pred. No. 1.7e-133;
Matches 298; Conservative 29; Mismatches 18; Indels 0; Gaps 0;

QY . 1 MSLFGLLVTALAGORRGTOAESNLSSKQFSSNKEQNGVQDPOHERIITVSTNGSIHS 60
Db 1 MLLGLLLTALAGQRTGTRAESNLSSKQLSSDKEQNGVQDPHRRVVTISNGSIHS 60
QY 61 PRFPHTYPRNTVLVRLVAIVENVMVQLTDFRFGLEDPEDDICKYDFVEVEEPSDGTIL 120
Db- 61 PRFPHTYPRNTVLVRLVAIVENVMVQLTDFRFGLEDPEDDICKYDFVEVEEPSDGSVL 120
QY 121 GRWCSGTVPGKQISKGNQIRFVSDVEYFPFSEPGFCIHYNVMPQTEAVSPSVLPSSA 180
Db 121 GRWCSGTVPGKQTSKGNHIRFVSDVEYFPFSEPGFCIHYSIIMPQVTTETSPSVLPSS 180
QY 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVGRKSRVVDLNL 240
Db 181 LSLLDNNNAVTAFTSEELIRYLEPDRWQVLDLSYKPTWQLLGKAFVGRKSKVNVNL 240
QY 241 LTEEVRVLSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300
Db 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
QY 301 VTKKYHEVLQRPKTVGRGLHSLTDVALEHHEECDCVCRGSTGG 345
Db 301 VTKKYHEVLQRPKTVGRGLHSLTDVALEHHEECDCVCRGNAGG 345

RESULT 5
Q9EQX6 PRELIMINARY; PRT; 345 AA.
AC Q9EQX6
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Spinal cord-derived growth factor.
GN Name=rsdggf;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalios D.E., Schmerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Mammary tumor;
RA Strassberg R.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
DR EMBL; BC037696; AAH37696.1; -.
DR HSSP; Q9JUS8; LNT0.
DR MGD; MGI:1859631; Pdgfc.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0005161; P:platelet-derived growth factor receptor bin. .; IDA.
DR GO; GO:0008284; P:positive regulation of cell proliferation; IDA.
DR GO; GO:0050730; P:regulation of peptidyl-tyrosine phosphoryla. .; IDA.
DR GO; GO:0007171; P:transmembrane receptor protein tyrosine kin. .; IDA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00341; PDGF; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF_2; 1.
DR Growth factor; Mitogen.
SQ SEQUENCE 345 AA; 38741 MW; 9A58A05C6C0E9614 CRC64;

Query Match 89.5%; Score 1662; DB 2; Length 345;
Best Local Similarity 86.4%; Pred. No. 1.7e-133;
Matches 298; Conservative 29; Mismatches 18; Indels 0; Gaps 0;

QY . 1 MSLFGLLVTALAGORRGTOAESNLSSKQFSSNKEQNGVQDPOHERIITVSTNGSIHS 60
Db 1 MLLGLLLTALAGQRTGTRAESNLSSKQLSSDKEQNGVQDPHRRVVTISNGSIHS 60
QY 61 PRFPHTYPRNTVLVRLVAIVENVMVQLTDFRFGLEDPEDDICKYDFVEVEEPSDGTIL 120
Db- 61 PRFPHTYPRNTVLVRLVAIVENVMVQLTDFRFGLEDPEDDICKYDFVEVEEPSDGSVL 120
QY 121 GRWCSGTVPGKQISKGNQIRFVSDVEYFPFSEPGFCIHYNVMPQTEAVSPSVLPSSA 180
Db 121 GRWCSGTVPGKQTSKGNHIRFVSDVEYFPFSEPGFCIHYSIIMPQVTTETSPSVLPSS 180
QY 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVGRKSRVVDLNL 240
Db 181 LSLLDNNNAVTAFTSEELIRYLEPDRWQVLDLSYKPTWQLLGKAFVGRKSKVNVNL 240
QY 241 LTEEVRVLSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300
Db 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
QY 301 VTKKYHEVLQRPKTVGRGLHSLTDVALEHHEECDCVCRGSTGG 345
Db 301 VTKKYHEVLQRPKTVGRGLHSLTDVALEHHEECDCVCRGNAGG 345

RESULT 5
Q9EQX6 PRELIMINARY; PRT; 345 AA.
AC Q9EQX6
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Spinal cord-derived growth factor.
GN Name=rsdggf;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalios D.E., Schmerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Mammary tumor;
RA Strassberg R.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
DR EMBL; BC037696; AAH37696.1; -.
DR HSSP; Q9JUS8; LNT0.
DR MGD; MGI:1859631; Pdgfc.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0005161; P:platelet-derived growth factor receptor bin. .; IDA.
DR GO; GO:0008284; P:positive regulation of cell proliferation; IDA.
DR GO; GO:0050730; P:regulation of peptidyl-tyrosine phosphoryla. .; IDA.
DR GO; GO:0007171; P:transmembrane receptor protein tyrosine kin. .; IDA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00341; PDGF; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF_2; 1.
DR Growth factor; Mitogen.
SQ SEQUENCE 345 AA; 38741 MW; 9A58A05C6C0E9614 CRC64;

Query Match 89.5%; Score 1662; DB 2; Length 345;
Best Local Similarity 86.4%; Pred. No. 1.7e-133;
Matches 298; Conservative 29; Mismatches 18; Indels 0; Gaps 0;

QY . 1 MSLFGLLVTALAGORRGTOAESNLSSKQFSSNKEQNGVQDPOHERIITVSTNGSIHS 60
Db 1 MLLGLLLTALAGQRTGTRAESNLSSKQLSSDKEQNGVQDPHRRVVTISNGSIHS 60
QY 61 PRFPHTYPRNTVLVRLVAIVENVMVQLTDFRFGLEDPEDDICKYDFVEVEEPSDGTIL 120
Db- 61 PRFPHTYPRNTVLVRLVAIVENVMVQLTDFRFGLEDPEDDICKYDFVEVEEPSDGSVL 120
QY 121 GRWCSGTVPGKQISKGNQIRFVSDVEYFPFSEPGFCIHYNVMPQTEAVSPSVLPSSA 180
Db 121 GRWCSGTVPGKQTSKGNHIRFVSDVEYFPFSEPGFCIHYSIIMPQVTTETSPSVLPSS 180
QY 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVGRKSRVVDLNL 240
Db 181 LSLLDNNNAVTAFTSEELIRYLEPDRWQVLDLSYKPTWQLLGKAFVGRKSKVNVNL 240
QY 241 LTEEVRVLSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300
Db 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
QY 301 VTKKYHEVLQRPKTVGRGLHSLTDVALEHHEECDCVCRGSTGG 345
Db 301 VTKKYHEVLQRPKTVGRGLHSLTDVALEHHEECDCVCRGNAGG 345

RESULT 5
Q9EQX6 PRELIMINARY; PRT; 345 AA.
AC Q9EQX6
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Spinal cord-derived growth factor.
GN Name=rsdggf;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalios D.E., Schmerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Mammary tumor;
RA Strassberg R.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
DR EMBL; BC037696; AAH37696.1; -.
DR HSSP; Q9JUS8; LNT0.
DR MGD; MGI:1859631; Pdgfc.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0005161; P:platelet-derived growth factor receptor bin. .; IDA.
DR GO; GO:0008284; P:positive regulation of cell proliferation; IDA.
DR GO; GO:0050730; P:regulation of peptidyl-tyrosine phosphoryla. .; IDA.
DR GO; GO:0007171; P:transmembrane receptor protein tyrosine kin. .; IDA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00341; PDGF; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF_2; 1.
DR Growth factor; Mitogen.
SQ SEQUENCE 345 AA; 38741 MW; 9A58A05C6C0E9614 CRC64;

Query Match 88.6%; Score 1646; DB 2; Length 345;
Best Local Similarity 85.5%; Pred. No. 4e-132;
Matches 295; Conservative 30; Mismatches 20; Indels 0; Gaps 0;

QY 1 MSLFGLLVTALAGORRGTOAESNLSSKQFSSNKEQNGVQDPOHERIITVSTNGSIHS 60
Db 1 MLLGLLLTALAGQRTGTRAESNLSSKQLSSDKEQNGVQDPHRRVVTISNGSIHS 60
QY 61 PRFPHTYPRNTVLVRLVAIVENVMVQLTDFRFGLEDPEDDICKYDFVEVEEPSDGTIL 120
Db 61 PRFPHTYPRNTVLVRLVAIVENVMVQLTDFRFGLEDPEDDICKYDFVEVEEPSDGSVL 120
QY 121 GRWCSGTVPGKQISKGNQIRFVSDVEYFPFSEPGFCIHYNVMPQTEAVSPSVLPSSA 180
Db 121 GRWCSGTVPGKQTSKGNHIRFVSDVEYFPFSEPGFCIHYSIIMPQVTTETSPSVLPSSA 180
QY 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVGRKSRVVDLNL 240
Db 181 LSLLDNNNAVTAFTSEELIRYLEPDRWQVLDLSYKPTWQLLGKAFVGRKSKVNVNL 240
QY 241 LTEEVRVLSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300
Db 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
QY 301 VTKKYHEVLQRPKTVGRGLHSLTDVALEHHEECDCVCRGSTGG 345
Db 301 VTKKYHEVLQRPKTVGRGLHSLTDVALEHHEECDCVCRGNTEG 345

RESULT 6
Q9JHV8 PRELIMINARY; PRT; 345 AA.
AC Q9JHV8
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Platelet-derived growth factor C.
GN Name=pdgfc;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss-Webster/NIH;
RX MEDLINE=20417814; PubMed=10960785; DOI=10.1016/S0925-4773(00)00425-1;
RA Ding H., Wu X., Kim I., Tam P.P.L., Koh G.Y., Nagy A.;
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DR PROSITE; PS0278; PDGF_2; 1.
FT NON_TER 1
FT NON_TER 258
SQ SEQUENCE 258 AA; 29255 MW; 88625B989FCC3F8B CRC64;

Query Match 67.8%; Score 1260; DB 2; Length 258;
Best Local Similarity 85.6%; Pred. No. 2.6e-99;
Matches 220; Conservative 25; Mismatches 12; Indels 0; Gaps 0;

QY 42 QDQHERIITVSTNGSIHSPRPHTYPRNTVLVWLVAEENVTQLTDFRFGLEDPE 101
Db 1 QDQHERVVTISGNSIHSKPEPHYPRNTVLVWLVAEENVTQLTDFRFGLEDPE 60

QY 102 DICKYDFVEVEPSDGTILGRWCGSTVPGKQISGNQIRIRFVSDYFPPSPGCIHYN 161
Db 61 DICKYDFVEVEPSDGTILGRWCGSTVPGKQISGNQIRIRFVSDYFPPSPGCIHYS 120

QY 162 IVMPOFTVAVSVLPSPGALPDLNNATFSTLEDLIRYLEPERWOLDLEDLYRPTWQ 221
Db 121 IIMPQVTTTSVLPSPGALSJDLNNATFSTVEELIRFLEPRWQIDLSLYKPTWP 180

QY 222 LIGKAFVGRKRVVDLNLTEBEVLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCG 281
Db 181 LIGKAFVGRKRVVDLNLTEBEVLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCG 240

QY 282 GNCACCLHNCNECQVCP 298
Db 241 GNCACCLHNCNECQVCP 257

RESULT 9
QSGZPO ID Q9GZP0 PRELIMINARY; PRT; 370 AA.
AC Q9GZP0;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Spinal cord-derived growth factor-B (MSTP036) (Platelet-derived growth
DE factor D) (iris-expressed growth factor long form).
GN Name=hSCDGF-B; Synonyms=IEGF, PDGFD;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21092670; PubMed=11162582; DOI=10.1006/bbrc.2000.4187;
RA Hamada T., Ui-Tei K., Imaki J., Miyata Y.;
RT "Molecular cloning of SCDGF-B, a novel growth factor homologous to
RT SCDGF/PDGF-C/fallotein.";
RL Biochem. Biophys. Res. Commun. 280:733-737(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Aorta;
RA Liu B., Liu Y.Q., Wang X.Y., Zhao B., Sheng H., Zhao X.W., Liu S.,
RA Xu Y.Y., Ye J., Song L., Gao Y., Zhang C.L., Zhang J., Wei Y.J.,
RA Cao H.Q., Zhao Y., Liu L.S., Ding J.F., Gao R.L., Wu Q.Y., Qiang B.Q.,
RA Yuan J.G., Liew C.C., Zhao M.S., Hui R.T.;
RL Submitted (DEC-1998) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21231380; PubMed=11331882; DOI=10.1038/35074593;
RA LaRoche W.J., Jeffers M., McDonald W.F., Chilla K.R.A.,
RA Giese N.A., Lokker N.A., Sullivan C., Boldog F.B., Yang M., Vernet C.,
RA Burgess C.B., Fernandez E., Degler L.L., Rittman B., Shinkets J.,
RA Shinkets R.A., Rothberg J.M., Lichenstein H.S.;
RT "PDGF D, A Novel Protease-Activated Growth Factor.";
RL Nat. Cell Biol. 3:517-521(2001).
RN [4]
RP SEQUENCE FROM N.A.
RX PubMed=11331881; DOI=10.1038/35074588;
RA Bergsten E., Uutela M., Li X., Pietras K., Ostman A., Heidin C.H.,
RA Alitalo K., Eriksson U.;
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RT "PDGF-D is a specific, protease-activated ligand for the PDGF beta-
RT receptor.";
RL Nat. Cell Biol. 3:512-516(2001).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Iris;
RX MEDLINE=22103462; PubMed=12107412;
RA Wistow G., Berse G., Smith D., Peterson K.;
RA Bouffard G., Smith D., Peterson K.;
RT "Expressed sequence tag analysis of adult human iris for the NEIBank
RT project: steroid-response factors and similarities with retinal
RT pigment epithelium";
RL Mol. Vision 8:185-195(2002).
DR EMBL; AB033832; BAB18903.1; -
DR EMBL; AF113216; AAG39287.1; -
DR EMBL; AF335584; AAK38840.1; -
DR EMBL; AF336376; AAK56136.1; -
DR EMBL; AY027517; AAK20081.1; -
DR PIR; JC7591; JC7591.
DR HSP; Q9JUS8; IN70.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD growth factor.
DR InterPro; IPR010916; TONB_Box_N.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS02078; PDGF_2; 1.
DR PROSITE; PS00430; TONB_DEPENDENT_REC_1; UNKNOWN 1.
DR SEQUENCE 370 AA; 42848 MW; D387F485E7BB7674_CRC64;

Query Match 39.9%; Score 741.5; DB 2; Length 370;
Best Local Similarity 43.6%; Pred. No. 8.1e-55;
Matches 159; Conservative 59; Mismatches 114; Indels 33; Gaps 10;

QY 3 LFGLLVTSALAGQRRGTQAESNLSSKQFSSN---KEQNGVQD-PQHERIITVSTNGSI 58
Db 5 IFVYTLICANFCSCRDTSATPSASIKALRNANLRDESNHLLTDLRYRDETIOVKGNGYV 64

QY 59 HSPRPHTYPRNTVLVWLVAEENVTQLTDFRFGLEDPEDDICKYDFVEVEPSDGT 118
Db 65 QSPRPNSYPRNLLTWRLHS-QENTRIQLVDFDQFGLAEANDICRTDFVEVEDISETS 123

QY 119 --ILGRWCGSTVPGKQISGNQIRIRFVSDYFPPSPGFCIHYNVMPQFTEAV----- 171
Db 124 TIIRGWCHEVPPRIKSRNQIKITFKSDDYFAKPGFKIYYSYL-LEDQPAASSETN 182

QY 172 -----SPSVLPSPGALPDLNNATFSTLEDLIRYLEPERWOLDLEDLYR 217
Db 183 WESVTSISGVSNSPSVTDPT-LIADALDKIAEFDTVEDLLKYFPNPSQEDLENNYL 241

QY 218 PTWOLLGKAFVGRKRVVDLNLTEBEVLYSCTPRNFSVSIREELKRTDTTFWPGCLLV 277
Db 242 DTPRGRKSY-HDRASK-VLDRLNNDKAKYSCIPRYSVNIIRBELKLANVVFPRCLLV 299

QY 278 KRCGNCACCLHNCNECQVPSKTKYVQLQRP---KTGVRGLHKSLLTDVALEHHEE 334
Db 300 QRCGNCGCGTVNWRSCNCSGKTKYVQLQRP---KTGVRGLHKSLLTDVALEHHEE 359

QY 335 CDCVC 339
Db 360 CDCIC 364

RESULT 10
Q9BWV5 ID Q9BWV5 PRELIMINARY; PRT; 364 AA.
AC Q9BWV5;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
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Db          258 GIEV 261
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RESULT 15
NRPI BRARE
ID NRPI BRARE STANDARD; PRT; 923 AA.
AC Q8QF6; Q8AXP1;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Neuropilin-1 precursor (znrp1).
GN Name=nrp1; Synonyms=up-1;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, AND DEVELOPMENTAL STAGE.
RC STRAIN=AB; TISSUE=Embryo;
RX Pubmed=12142468; DOI=10.1073/pnas.162366299;
RA Lee P., Golshi K., Davidson A.J., Mannix R., Zon L., Klagsbrun M.;
RT "Neuropilin-1 is required for vascular development and is a mediator
of VEGF-dependent angiogenesis in zebrafish.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:10470-10475(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Shoji W., Tawarayama H.;
RT "The cloning and expression of neuropilin-1.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor involved in the development of the
cardiovascular system, in angiogenesis, in the formation of
certain neuronal circuits and in organogenesis outside the nervous
system. It mediates the chemorepulsant activity of semaphorins.
CC Regulates angiogenesis through a VEGF-dependent pathway.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- DEVELOPMENTAL STAGE: Expressed both maternally and zygotically.
Maternal transcripts are widely expressed until the early gastrula
stage, then become localized to the yolk syncytial layer. During
somatogenesis and later stages of development, expression occurs
mainly in neuronal and vascular tissues.
CC -!- SIMILARITY: Belongs to the neuropilin family.
CC -!- SIMILARITY: Contains 2 CUB domains.
CC -!- SIMILARITY: Contains 2 F5/8 type C domains.
CC -!- SIMILARITY: Contains 1 MAM domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC
CC EMBL; AY064213; RAL40862.1; -.
CC EMBL; AB088776; BAC53657.1; -.
CC HSSP; O14786; IKEX.
CC ZFIN; ZDB-GENE-030519-2; nrp1.
CC InterPro; IPR000859; CUB.
CC InterPro; IPR000421; FAS8 C.
CC InterPro; IPR008979; Gal_Bind_like.
CC InterPro; IPR000998; MAM.
CC Pfam; PF00431; CUB; 2.
CC Pfam; PF00754; F5_F8_type_C; 2.
CC Pfam; PF00629; MAM; 1.
CC SMART; SM00042; CUB; 2.
CC SMART; SM00231; FAS8C; 2.
CC SMART; SM00137; MAM; 1.
CC PROSITE; PS01180; CUB; 2.
CC PROSITE; PS01285; FAS8C_1; 1.
CC PROSITE; PS01286; FAS8C_2; 2.
CC PROSITE; PS50022; FAS8C_3; 2.

DR PROSITE; PS00740; MAM_1; 1.
DR PROSITE; PS50060; MAM_2; 1.
KW Angiogenesis; Glycoprotein; Neurogenesis; Receptor; Repeat; Signal;
KW Transmembrane.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 923 Neuropilin-1.
FT DOMAIN 20 856 Extracellular (Potential).
FT TRANSMEM 857 877 Potential.
FT DOMAIN 878 923 Cytoplasmic (Potential).
FT DOMAIN 145 139 CUB 1.
FT DOMAIN 145 263 CUB 2.
FT DOMAIN 273 422 F5/8 type C 1.
FT DOMAIN 429 581 F5/8 type C 2.
FT DOMAIN 642 811 MAM.
FT DISULFID 25 52 Probable.
FT DISULFID 80 102 Probable.
FT DISULFID 145 171 Probable.
FT DISULFID 204 226 Probable.
FT DISULFID 273 422 By similarity.
FT DISULFID 429 581 By similarity.
FT CARBOHYD 148 148 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 259 259 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 520 520 N-linked (GlcNAc...) (Potential).
FT CONFLICT 230 230 T -> S (in Ref. 2).
FT CONFLICT 317 317 K -> E (in Ref. 2).
FT CONFLICT 454 454 T -> S (in Ref. 2).
FT CONFLICT 463 617 L -> M (in Ref. 2).
FT CONFLICT 617 617 G -> D (in Ref. 2).
SQ SEQUENCE 923 AA; 102492 MW; 2ED84B129AA92B2D CRC64;

Query Match 10.3%; Score 190.5; DB 1; Length 923;
Best Local Similarity 27.6%; Pred. No. 3e-07; Mismatches 29; Indels 49; Gaps 8;
Matches 66; Conservative 29;

QY 5 GLLVTSALAGQRCTQAEISLSSKFPQSSNKEQNGVQDPQHERIITVTNGSIHSRPP 64
DB 12 GFLIVSALKNDKCGDN-----IRTSANYLTPGVP 43
QY 65 HTYPRNTVLVRLVAEENVMQLTDFRFGLEDDEDDICKYDFVEVEPSD--GTLGR 122
DB 44 VSYTPSQKCIWITAPGPNQRLINFNPHFLEDR---CKDYVVEVRDGVDENGQLVGK 100
QY 123 WCGSGTVPGKOLISGNQIRIRFVSDEYFPSPGFCIHYNVMP-----QFTEAVSPSVL 176
DB 101 YCGK-IAPSPVSSGNQLFIKPVSD-YETHGAGSIRYEIPKYGECSENFSS--SSGVI 156
QY 177 PPSALPLDLLNNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWOLGKAFVGRKSRV 235
DB 157 KSPGPFKEKYPNNLDCTFMIFAPKMSIIVLEFESPELEPDTQP-----PAGVFCRYDL 209

Search completed: September 3, 2005, 19:29:41
Job time : 117.5 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 3, 2005, 19:19:05 ; Search time 30 Seconds
(without alignments)
858.464 Million cell updates/sec

Title: US-09-818-943-1
Perfect score: 1558
Sequence: 1 MSFGLLLVTSALAGRRGT.....DVALEHHECDVCVRGSGTG 345

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_AA.*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pap.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pap.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pap.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pap.*
- 5: /cgn2_6/ptodata/1/iaa/PTCUS_COMB.pap.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1851	99.6	345	US-09-040-220D-2	Sequence 2, Appli
2	1851	99.6	345	US-09-457-086-2	Sequence 2, Appli
3	1851	99.6	345	US-09-265-686-2	Sequence 2, Appli
4	1851	99.6	345	US-09-540-224-5	Sequence 5, Appli
5	1851	99.6	345	US-09-564-595D-33	Sequence 33, Appli
6	1851	99.6	345	US-09-706-968-2	Sequence 2, Appli
7	1851	99.6	345	US-09-723-749-2	Sequence 2, Appli
8	1851	99.6	345	US-09-823-033-2	Sequence 2, Appli
9	1851	99.6	345	US-09-468-647A-101	Sequence 101, App
10	1851	99.6	345	US-09-468-647A-110	Sequence 110, App
11	1851	99.6	345	US-09-468-647A-130	Sequence 130, App
12	1851	99.6	345	US-10-139-583-2	Sequence 2, Appli
13	1851	99.6	374	US-09-468-647A-118	Sequence 118, App
14	1843	99.2	345	US-09-468-647A-2	Sequence 2, Appli
15	1843	99.2	345	US-09-468-647A-103	Sequence 103, App
16	1757	94.6	355	US-09-468-647A-122	Sequence 122, App
17	1755	94.5	354	US-09-468-647A-120	Sequence 120, App
18	1747	94.0	323	US-09-468-647A-1	Sequence 1, Appli
19	1664	89.6	345	US-09-457-066-43	Sequence 43, Appli
20	1664	89.6	345	US-09-564-595D-35	Sequence 35, Appli
21	1664	89.6	345	US-09-706-968-43	Sequence 43, Appli
22	1664	89.6	345	US-09-823-033-4	Sequence 4, Appli
23	1664	89.6	345	US-10-139-583-43	Sequence 43, Appli
24	1443	5	77.7	US-09-468-647A-112	Sequence 112, App
25	1325	71.3	302	US-09-564-595D-54	Sequence 54, Appli
26	1266.5	68.2	303	US-09-564-595D-57	Sequence 57, Appli
27	1098	59.1	316	US-09-564-595D-55	Sequence 55, Appli

28	1051.5	56.6	317	4	US-09-564-595D-56	Sequence 56, Appli
29	807	43.4	167	4	US-09-468-647A-111	Sequence 111, App
30	806	43.4	168	4	US-09-468-647A-27	Sequence 27, Appli
31	806	43.4	168	4	US-09-468-647A-126	Sequence 126, App
32	741.5	39.9	370	4	US-09-457-066-37	Sequence 37, Appli
33	741.5	39.9	370	4	US-09-540-224-2	Sequence 2, Appli
34	741.5	39.9	370	4	US-09-564-595D-2	Sequence 2, Appli
35	741.5	39.9	370	4	US-09-706-968-37	Sequence 37, Appli
36	741.5	39.9	370	4	US-09-808-972-2	Sequence 2, Appli
37	741.5	39.9	370	4	US-09-823-033-5	Sequence 5, Appli
38	741.5	39.9	370	4	US-09-438-046-8	Sequence 8, Appli
39	741.5	39.9	370	4	US-10-139-583-37	Sequence 37, Appli
40	741.5	39.9	370	4	US-10-039-847A-2	Sequence 2, Appli
41	739.5	39.8	322	4	US-09-438-046-6	Sequence 6, Appli
42	737.5	39.7	370	4	US-09-540-224-4	Sequence 4, Appli
43	737.5	39.7	370	4	US-09-564-595D-53	Sequence 53, Appli
44	737.5	39.7	370	4	US-09-808-972-4	Sequence 4, Appli
45	737.5	39.7	370	4	US-10-039-847A-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-040-220D-2
; Sequence 2, Application US/09040220D
; Patent No. 6391311
; GENERAL INFORMATION:
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Kuo, Sophia S.
; TITLE OF INVENTION: NOVEL POLYPEPTIDES HAVING HOMOLOGY TO VASCULAR
; TITLE OF INVENTION: ENDOTHELIAL CELL GROWTH FACTOR AND BONE MORPHOGENETIC
; TITLE OF INVENTION: PROTEIN 1 AND NUCLEIC ACIDS ENCODING SAME, THEIR USES,
; TITLE OF INVENTION: AND PROCESSES FOR THEIR PRODUCTION
; FILE REFERENCE: P1122
; CURRENT APPLICATION NUMBER: US/09/040,220D
; CURRENT FILING DATE: 1998-03-17
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Human
US-09-040-220D-2

Query Match	99.6%	Score 1851;	DB 3;	Length 345;
Best Local Similarity	99.4%	Pred. No. 8.3e-193;		
Matches 343;	Conservative 2;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MSFGLLLVTSALAGRRGTQAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS	60	
Db	1	MSFGLLLVTSALAGRRGTQAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS	60	
Qy	61	PRPHTYPRNTVLVWRLVAVEENVWVQLTDEREGLEDPRDDICKYDFVEVEEPSDGTIL	120	
Db	61	PRPHTYPRNTVLVWRLVAVEENVWVQLTDEREGLEDPRDDICKYDFVEVEEPSDGTIL	120	
Qy	121	GRWCGSGTVFGKQISKGNQIRFVSDYFSEPGFCIHYNVMPQTEAVSPVLPESA	180	
Db	121	GRWCGSGTVFGKQISKGNQIRFVSDYFSEPGFCIHYNVMPQTEAVSPVLPESA	180	
Qy	181	LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYPTWQLLKAFVFGKRSRVDLNL	240	
Db	181	LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYPTWQLLKAFVFGKRSRVDLNL	240	
Qy	241	LTEVRVLYSCTPRNFSVSIREELKRTDTIWPFGCLLVKRCGGNCACCLHNCNECQVPSK	300	
Db	241	LTEVRVLYSCTPRNFSVSIREELKRTDTIWPFGCLLVKRCGGNCACCLHNCNECQVPSK	300	
Qy	301	VTKKYHEVLQRLPKTGVGRGLHKSITDVALEHHEECDCVCRGSGTG 345		
Db	301	VTKKYHEVLQRLPKTGVGRGLHKSITDVALEHHEECDCVCRGSGTG 345		

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RESULT 2
US-09-457-066-2
; Sequence 2, Application US/09457066
; Patent No. 6432673
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/09/457,066
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-457-066-2

Query Match      99.6%; Score 1851; DB 4; Length 345;
Best Local Similarity 99.4%; Pred. No. 8.3e-193;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLFGLLLVTSALAGQRGTQAESNLSSKQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60
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DB 61 PRFPHTYPRNTVLVRLVAEENWVIQLTDFRFGLEDPEDDICKYDFVEVEEPSDGTIL 120
QY 121 GRWCGSGTVPKGQISKGNQIRIRFVSDDEYFPSEPGFCIHYNIVMPQFTEAVSPVLPPSA 180
DB 121 GRWCGSGTVPKGQISKGNQIRIRFVSDDEYFPSEPGFCIHYNIVMPQFTEAVSPVLPPSA 180
QY 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLIRPTWQLLGKAFVFGRSRVVDLNL 240
DB 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLIRPTWQLLGKAFVFGRSRVVDLNL 240
QY 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300
DB 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300
QY 301 VTKKYHEVLQRPKTGVRGLHKSITDVALEHHEECDCVCRGSTGG 345
DB 301 VTKKYHEVLQRPKTGVRGLHKSITDVALEHHEECDCVCRGSTGG 345

RESULT 4
US-09-540-224-5
; Sequence 5, Application US/09540224
; Patent No. 6468543
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: Hart, Charles E.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4
; FILE REFERENCE: 00-28
; CURRENT APPLICATION NUMBER: US/09/540,224
; CURRENT FILING DATE: 2000-03-31
; EARLIER APPLICATION NUMBER: US 60/180,169
; EARLIER FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-540-224-5

Query Match      99.6%; Score 1851; DB 4; Length 345;
Best Local Similarity 99.4%; Pred. No. 8.3e-193;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MSLFGLLLVTSALAGQRGTQAESNLSSKQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60
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DB 61 PRFPHTYPRNTVLVRLVAEENWVIQLTDFRFGLEDPEDDICKYDFVEVEEPSDGTIL 120
QY 121 GRWCGSGTVPKGQISKGNQIRIRFVSDDEYFPSEPGFCIHYNIVMPQFTEAVSPVLPPSA 180
DB 121 GRWCGSGTVPKGQISKGNQIRIRFVSDDEYFPSEPGFCIHYNIVMPQFTEAVSPVLPPSA 180
QY 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLIRPTWQLLGKAFVFGRSRVVDLNL 240
DB 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLIRPTWQLLGKAFVFGRSRVVDLNL 240
QY 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300
DB 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300
QY 301 VTKKYHEVLQRPKTGVRGLHKSITDVALEHHEECDCVCRGSTGG 345
DB 301 VTKKYHEVLQRPKTGVRGLHKSITDVALEHHEECDCVCRGSTGG 345

RESULT 3
US-09-265-686-2
; Sequence 2, Application US/09265686
; Patent No. 6455283
; GENERAL INFORMATION:
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Kuo, Sophia S.
; TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND BMPI
; FILE REFERENCE: P1122P2
; CURRENT APPLICATION NUMBER: US/09/265,686
; CURRENT FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: US 09/040,220
; PRIOR FILING DATE: 1998-03-17
; PRIOR APPLICATION NUMBER: US 09/184,216
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Human
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US-09-265-686-2

Query Match      99.6%; Score 1851; DB 4; Length 345;
Best Local Similarity 99.4%; Pred. No. 8.3e-193;
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DB 61 PRFPHTYPRNTVLVRLVAEENWVIQLTDFRFGLEDPEDDICKYDFVEVEEPSDGTIL 120
QY 121 GRWCGSGTVPKGQISKGNQIRIRFVSDDEYFPSEPGFCIHYNIVMPQFTEAVSPVLPPSA 180
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DB 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLIRPTWQLLGKAFVFGRSRVVDLNL 240
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DB 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300
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DB 301 VTKKYHEVLQRPKTGVRGLHKSITDVALEHHEECDCVCRGSTGG 345

RESULT 4
US-09-540-224-5
; Sequence 5, Application US/09540224
; Patent No. 6468543
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: Hart, Charles E.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4
; FILE REFERENCE: 00-28
; CURRENT APPLICATION NUMBER: US/09/540,224
; CURRENT FILING DATE: 2000-03-31
; EARLIER APPLICATION NUMBER: US 60/180,169
; EARLIER FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-540-224-5

Query Match      99.6%; Score 1851; DB 4; Length 345;
Best Local Similarity 99.4%; Pred. No. 8.3e-193;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLFGLLLVTSALAGQRGTQAESNLSSKQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60
DB 1 MSLFGLLLVTSALAGQRGTQAESNLSSKQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60
QY 61 PRFPHTYPRNTVLVRLVAEENWVIQLTDFRFGLEDPEDDICKYDFVEVEEPSDGTIL 120
DB 61 PRFPHTYPRNTVLVRLVAEENWVIQLTDFRFGLEDPEDDICKYDFVEVEEPSDGTIL 120
QY 121 GRWCGSGTVPKGQISKGNQIRIRFVSDDEYFPSEPGFCIHYNIVMPQFTEAVSPVLPPSA 180
DB 121 GRWCGSGTVPKGQISKGNQIRIRFVSDDEYFPSEPGFCIHYNIVMPQFTEAVSPVLPPSA 180
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DB 301 VTKKYHEVLQRPKTGVRGLHKSITDVALEHHEECDCVCRGSTGG 345
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QY 301 VTKKYHEVLQRPKTVGRLHKLSTDLVALEHHEECDCVCRGSTGG 345
Db 301 VTKKYHEVLQRPKTVGRLHKLSTDLVALEHHEECDCVCRGSTGG 345

RESULT 5

US-09-564-595D-33
; Sequence 33, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 345
; TYPE: PRP
; ORGANISM: Homo sapiens
US-09-564-595D-33

Query Match 99.6%; Score 1851; DB 4; Length 345;
Best Local Similarity 99.4%; Pred. No. 8.3e-193;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MSLFGLLLVTSALAGQRRGTQAESNLSSKQFSSNKQNGVQDPOHERIITVSTNGSIHS 60
QY 61 PRPHTYPRNTVLVRLVAVEENVWIQLTFDERFGLDEPDDICKYDFVEVEEPSDGTIL 120
Db 61 PRPHTYPRNTVLVRLVAVEENVWIQLTFDERFGLDEPDDICKYDFVEVEEPSDGTIL 120
QY 121 GRWCGSTVPKGQISKGNQIRFVSDYFSPSEPGFCIHYNIVMPQTEAVSPVLPSPA 180
Db 121 GRWCGSTVPKGQISKGNQIRFVSDYFSPSEPGFCIHYNIVMPQTEAVSPVLPSPA 180
QY 181 LPDLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLGKAFVFGKRSRVVDLNL 240
Db 181 LPDLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLGKAFVFGKRSRVVDLNL 240
QY 241 LTEEVRLYSCPTPRNFVSIRBELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPVK 300
Db 241 LTEEVRLYSCPTPRNFVSIRBELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPVK 300
QY 301 VTKKYHEVLQRPKTVGRLHKLSTDLVALEHHEECDCVCRGSTGG 345
Db 301 VTKKYHEVLQRPKTVGRLHKLSTDLVALEHHEECDCVCRGSTGG 345

RESULT 6

US-09-706-968-2
; Sequence 2, Application US/09706968
; Patent No. 6528050
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.

; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60C1
; CURRENT APPLICATION NUMBER: US/09/706,968
; CURRENT FILING DATE: 2000-11-06
; PRIOR APPLICATION NUMBER: US/09/541,752
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PRP
; ORGANISM: Homo sapiens
US-09-706-968-2

Query Match 99.6%; Score 1851; DB 4; Length 345;
Best Local Similarity 99.4%; Pred. No. 8.3e-193;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLFGLLLVTSALAGQRRGTQAESNLSSKQFSSNKQNGVQDPOHERIITVSTNGSIHS 60
Db 1 MSLFGLLLVTSALAGQRRGTQAESNLSSKQFSSNKQNGVQDPOHERIITVSTNGSIHS 60
QY 61 PRPHTYPRNTVLVRLVAVEENVWIQLTFDERFGLDEPDDICKYDFVEVEEPSDGTIL 120
Db 61 PRPHTYPRNTVLVRLVAVEENVWIQLTFDERFGLDEPDDICKYDFVEVEEPSDGTIL 120
QY 121 GRWCGSTVPKGQISKGNQIRFVSDYFSPSEPGFCIHYNIVMPQTEAVSPVLPSPA 180
Db 121 GRWCGSTVPKGQISKGNQIRFVSDYFSPSEPGFCIHYNIVMPQTEAVSPVLPSPA 180
QY 181 LPDLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLGKAFVFGKRSRVVDLNL 240
Db 181 LPDLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLGKAFVFGKRSRVVDLNL 240
QY 241 LTEEVRLYSCPTPRNFVSIRBELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPVK 300
Db 241 LTEEVRLYSCPTPRNFVSIRBELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPVK 300
QY 301 VTKKYHEVLQRPKTVGRLHKLSTDLVALEHHEECDCVCRGSTGG 345
Db 301 VTKKYHEVLQRPKTVGRLHKLSTDLVALEHHEECDCVCRGSTGG 345

RESULT 7

US-09-723-749-2
; Sequence 2, Application US/09723749
; Patent No. 6620784
; GENERAL INFORMATION:
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Kuo, Sophia S.
; TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND BMP1
; FILE REFERENCE: P1122P2D1
; CURRENT APPLICATION NUMBER: US/09/723,749
; CURRENT FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: US 09/265,686
; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: US 09/040,220
; PRIOR FILING DATE: 1998-03-17
; PRIOR APPLICATION NUMBER: US 09/184,216
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PRP
; ORGANISM: Human
US-09-723-749-2

Query Match 99.6%; Score 1851; DB 4; Length 345;
Best Local Similarity 99.4%; Pred. No. 8.3e-193;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MSLFGLLLVTSALAGRCGTQAESNLSSKFQSSNKQNGVQDPOHERIITVSTNGSIHS 60
Db 1 MSLFGLLLVTSALAGRCGTQAESNLSSKFQSSNKQNGVQDPOHERIITVSTNGSIHS 60
QY 61 PRFPHTYPRNTVLVRLVAIVENVMIQLTFDRFGLDEPDDEICKYDFVEVEEPSDGTIL 120
Db 61 PRFPHTYPRNTVLVRLVAIVENVMIQLTFDRFGLDEPDDEICKYDFVEVEEPSDGTIL 120
QY 121 GRWCGSGTVPGKQISKGNIQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTAEVSPVLPPSA 180
Db 121 GRWCGSGTVPGKQISKGNIQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTAEVSPVLPPSA 180
QY 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
Db 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
QY 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300
Db 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300
QY 301 VTKKYHEVLQRPKTVGRGLHKS LTDVALEHHEBCDCVCRGSTGG 345
Db 301 VTKKYHEVLQRPKTVGRGLHKS LTDVALEHHEBCDCVCRGSTGG 345

RESULT 8
US-09-823-033-2
; Sequence 2, Application US/09823033
; Patent No. 6663870
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; LIGAMENT AND CARTILAGE
; FILE REFERENCE: 00-12
; CURRENT APPLICATION NUMBER: US/09/823,033
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PRN
; ORGANISM: Homo sapiens
US-09-823-033-2

Query Match 99.6%; Score 1851; DB 4; Length 345;
Best Local Similarity 99.4%; Pred. No. 8.3e-193;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLFGLLLVTSALAGRCGTQAESNLSSKFQSSNKQNGVQDPOHERIITVSTNGSIHS 60
Db 1 MSLFGLLLVTSALAGRCGTQAESNLSSKFQSSNKQNGVQDPOHERIITVSTNGSIHS 60
QY 61 PRFPHTYPRNTVLVRLVAIVENVMIQLTFDRFGLDEPDDEICKYDFVEVEEPSDGTIL 120
Db 61 PRFPHTYPRNTVLVRLVAIVENVMIQLTFDRFGLDEPDDEICKYDFVEVEEPSDGTIL 120
QY 121 GRWCGSGTVPGKQISKGNIQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTAEVSPVLPPSA 180
Db 121 GRWCGSGTVPGKQISKGNIQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTAEVSPVLPPSA 180
QY 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
Db 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
QY 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300
Db 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300
QY 301 VTKKYHEVLQRPKTVGRGLHKS LTDVALEHHEBCDCVCRGSTGG 345
Db 301 VTKKYHEVLQRPKTVGRGLHKS LTDVALEHHEBCDCVCRGSTGG 345
```

```
RESULT 9
US-09-468-647A-101
; Sequence 101, Application US/09468647A
; Patent No. 6783953
; GENERAL INFORMATION:
; APPLICANT: Gordon, Robert D
; APPLICANT: Sprengel, Jorg J
; APPLICANT: Yon, Jeffery R
; APPLICANT: DiJkmans, Josiena J.H.
; APPLICANT: Gosiewska, Anna
; APPLICANT: Dhanaraj, Sridevi N
; APPLICANT: Xu, Jean
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-X
; FILE REFERENCE: BOL92.70011US00
; CURRENT APPLICATION NUMBER: US/09/468,647A
; CURRENT FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: GB 9828377.3
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: US 60/124,967
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: US 60/164,131
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 101
; LENGTH: 345
; TYPE: PRN
; ORGANISM: Homo sapiens
US-09-468-647A-101

Query Match 99.6%; Score 1851; DB 4; Length 345;
Best Local Similarity 99.4%; Pred. No. 8.3e-193;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLFGLLLVTSALAGRCGTQAESNLSSKFQSSNKQNGVQDPOHERIITVSTNGSIHS 60
Db 1 MSLFGLLLVTSALAGRCGTQAESNLSSKFQSSNKQNGVQDPOHERIITVSTNGSIHS 60
QY 61 PRFPHTYPRNTVLVRLVAIVENVMIQLTFDRFGLDEPDDEICKYDFVEVEEPSDGTIL 120
Db 61 PRFPHTYPRNTVLVRLVAIVENVMIQLTFDRFGLDEPDDEICKYDFVEVEEPSDGTIL 120
QY 121 GRWCGSGTVPGKQISKGNIQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTAEVSPVLPPSA 180
Db 121 GRWCGSGTVPGKQISKGNIQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTAEVSPVLPPSA 180
QY 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
Db 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
QY 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300
Db 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300
QY 301 VTKKYHEVLQRPKTVGRGLHKS LTDVALEHHEBCDCVCRGSTGG 345
Db 301 VTKKYHEVLQRPKTVGRGLHKS LTDVALEHHEBCDCVCRGSTGG 345

RESULT 10
US-09-468-647A-110
; Sequence 110, Application US/09468647A
; Patent No. 6783953
; GENERAL INFORMATION:
; APPLICANT: Gordon, Robert D
; APPLICANT: Sprengel, Jorg J
; APPLICANT: Yon, Jeffery R
; APPLICANT: DiJkmans, Josiena J.H.
; APPLICANT: Gosiewska, Anna
; APPLICANT: Dhanaraj, Sridevi N
; APPLICANT: Xu, Jean
```

; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-X
; FILE REFERENCE: B0192.70011US00
; CURRENT APPLICATION NUMBER: US/09/468,647A
; CURRENT FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: GB 9828377.3
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: US 60/124,967
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: US 60/164,131
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 110
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-468-647A-110

Query Match 99.6%; Score 1851; DB 4; Length 345;
Best Local Similarity 99.4%; Pred. No. 8.3e-193;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MSLFGLLLVTSALAGORRGTOAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS 60
Db 1 MSLFGLLLVTSALAGORRGTOAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS 60
Qy 61 PRPHTYPRNTLVWRLVAVEENVWVQLTDFERFGLDEPDDICKYDFVEVEEESDGTIL 120
Db 61 PRPHTYPRNTLVWRLVAVEENVWVQLTDFERFGLDEPDDICKYDFVEVEEESDGTIL 120
Qy 121 GRWCGSGTVPGKQISKGNQIRIRFVSDYFPSEPGFCIHYNIVMPQFTEAVSPVLPESA 180
Db 121 GRWCGSGTVPGKQISKGNQIRIRFVSDYFPSEPGFCIHYNIVMPQFTEAVSPVLPESA 180
Qy 181 LPDLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
Db 181 LPDLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
Qy 241 LTEEVRVLYSCTPRNFSVSIREEELKRTDTIIFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300
Db 241 LTEEVRVLYSCTPRNFSVSIREEELKRTDTIIFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300
Qy 301 VTKKYHEVLQRPKTVGRGLHKSITDVALEHHEBCDCVCRGSTGG 345
Db 301 VTKKYHEVLQRPKTVGRGLHKSITDVALEHHEBCDCVCRGSTGG 345

RESULT 11
US-09-468-647A-130
; Sequence 130, Application US/09468647A
; Patent No. 6783953
; GENERAL INFORMATION:
; APPLICANT: Gordon, Robert D
; APPLICANT: Sprengel, Jorg J
; APPLICANT: Yon, Jeffery R
; APPLICANT: Dijkmans, Josiena J.H.
; APPLICANT: Gosiewska, Anna
; APPLICANT: Dhanaraj, Sridevi N
; APPLICANT: Xu, Jean
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-X
; FILE REFERENCE: B0192.70011US00
; CURRENT APPLICATION NUMBER: US/09/468,647A
; CURRENT FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: GB 9828377.3
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: US 60/124,967
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: US 60/164,131
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 130
; LENGTH: 345

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-468-647A-130
Query Match 99.6%; Score 1851; DB 4; Length 345;
Best Local Similarity 99.4%; Pred. No. 8.3e-193;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MSLFGLLLVTSALAGORRGTOAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS 60
Db 1 MSLFGLLLVTSALAGORRGTOAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS 60
Qy 61 PRPHTYPRNTLVWRLVAVEENVWVQLTDFERFGLDEPDDICKYDFVEVEEESDGTIL 120
Db 61 PRPHTYPRNTLVWRLVAVEENVWVQLTDFERFGLDEPDDICKYDFVEVEEESDGTIL 120
Qy 121 GRWCGSGTVPGKQISKGNQIRIRFVSDYFPSEPGFCIHYNIVMPQFTEAVSPVLPESA 180
Db 121 GRWCGSGTVPGKQISKGNQIRIRFVSDYFPSEPGFCIHYNIVMPQFTEAVSPVLPESA 180
Qy 181 LPDLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
Db 181 LPDLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
Qy 241 LTEEVRVLYSCTPRNFSVSIREEELKRTDTIIFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300
Db 241 LTEEVRVLYSCTPRNFSVSIREEELKRTDTIIFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300
Qy 301 VTKKYHEVLQRPKTVGRGLHKSITDVALEHHEBCDCVCRGSTGG 345
Db 301 VTKKYHEVLQRPKTVGRGLHKSITDVALEHHEBCDCVCRGSTGG 345

RESULT 12
US-10-139-583-2
; Sequence 2, Application US/10139583
; Patent No. 6814965
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/10/139,583
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 09/457,066
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-139-583-2

Query Match 99.6%; Score 1851; DB 4; Length 345;
Best Local Similarity 99.4%; Pred. No. 8.3e-193;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MSLFGLLLVTSALAGORRGTOAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS 60
Db 1 MSLFGLLLVTSALAGORRGTOAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS 60
Qy 61 PRPHTYPRNTLVWRLVAVEENVWVQLTDFERFGLDEPDDICKYDFVEVEEESDGTIL 120
Db 61 PRPHTYPRNTLVWRLVAVEENVWVQLTDFERFGLDEPDDICKYDFVEVEEESDGTIL 120
Qy 121 GRWCGSGTVPGKQISKGNQIRIRFVSDYFPSEPGFCIHYNIVMPQFTEAVSPVLPESA 180
Db 121 GRWCGSGTVPGKQISKGNQIRIRFVSDYFPSEPGFCIHYNIVMPQFTEAVSPVLPESA 180

Db 121 GRWCGSGTVPKGQISKGNIQIRIRFVSDEYFSPGFCIHYNIVMPQFTEAVSPSVLPESA 180
Qy 181 LPDLNNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
Db 181 LPDLNNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
Qy 241 LTEEVRVLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300
Db 241 LTEEVRVLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300
Qy 301 VTKKYHEVLQRPKTVGRGLHKSITDVALEHHEECDCVCRGSTGG 345
Db 301 VTKKYHEVLQRPKTVGRGLHKSITDVALEHHEECDCVCRGSTGG 345

RESULT 13
US-09-468-647A-118
; Sequence 118, Application US/09468647A
; Patent No. 6783953
; GENERAL INFORMATION:
; APPLICANT: Gordon, Robert D
; APPLICANT: Sprengel, Jorg J
; APPLICANT: Yon, Jeffery R
; APPLICANT: Dijkmans, Josiena J.H.
; APPLICANT: Gosiewska, Anna
; APPLICANT: Dhanaraj, Sri devi N
; APPLICANT: Xu, Jean
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-X
; FILE REFERENCE: B0192.7001IUS00
; CURRENT APPLICATION NUMBER: US/09/468,647A
; CURRENT FILING DATE: 1999-12-21
; PRIOR FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: US 60/124,967
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: US 60/164,131
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 118
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-468-647A-118

Query Match 99.6%; Score 1851; DB 4; Length 374;
Best Local Similarity 99.4%; Pred. No. 9.4e-193;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MSLFGLLLVTSALAGORRGTOAESNLSSKQFSSNKEQNGVODPOHERIITVSTNGSIHS 60
Db 1 MSLFGLLLVTSALAGORRGTOAESNLSSKQFSSNKEQNGVODPOHERIITVSTNGSIHS 60
Qy 61 PRPHTYPRNTVLVWRLVAEENVWIQLTFDERFGLDEPDDICKYDFVEVEEPSDGTIL 120
Db 61 PRPHTYPRNTVLVWRLVAEENVWIQLTFDERFGLDEPDDICKYDFVEVEEPSDGTIL 120
Qy 121 GRWCGSGTVPKGQISKGNIQIRIRFVSDEYFSPGFCIHYNIVMPQFTEAVSPSVLPESA 180
Db 121 GRWCGSGTVPKGQISKGNIQIRIRFVSDEYFSPGFCIHYNIVMPQFTEAVSPSVLPESA 180
Qy 181 LPDLNNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
Db 181 LPDLNNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
Qy 241 LTEEVRVLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300
Db 241 LTEEVRVLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300
Qy 301 VTKKYHEVLQRPKTVGRGLHKSITDVALEHHEECDCVCRGSTGG 345
Db 301 VTKKYHEVLQRPKTVGRGLHKSITDVALEHHEECDCVCRGSTGG 345

RESULT 14
US-09-468-647A-2
; Sequence 2, Application US/09468647A
; Patent No. 6783953
; GENERAL INFORMATION:
; APPLICANT: Gordon, Robert D
; APPLICANT: Sprengel, Jorg J
; APPLICANT: Yon, Jeffery R
; APPLICANT: Dijkmans, Josiena J.H.
; APPLICANT: Gosiewska, Anna
; APPLICANT: Dhanaraj, Sri devi N
; APPLICANT: Xu, Jean
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-X
; FILE REFERENCE: B0192.7001IUS00
; CURRENT APPLICATION NUMBER: US/09/468,647A
; CURRENT FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: GB 9828377.3
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: US 60/124,967
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: US 60/164,131
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-468-647A-2

Query Match 99.2%; Score 1843; DB 4; Length 345;
Best Local Similarity 99.1%; Pred. No. 6.2e-192;
Matches 342; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MSLFGLLLVTSALAGORRGTOAESNLSSKQFSSNKEQNGVODPOHERIITVSTNGSIHS 60
Db 1 MSLFGLLLVTSALAGORRGTOAESNLSSKQFSSNKEQNGVODPOHERIITVSTNGSIHS 60
Qy 61 PRPHTYPRNTVLVWRLVAEENVWIQLTFDERFGLDEPDDICKYDFVEVEEPSDGTIL 120
Db 61 PRPHTYPRNTVLVWRLVAEENVWIQLTFDERFGLDEPDDICKYDFVEVEEPSDGTIL 120
Qy 121 GRWCGSGTVPKGQISKGNIQIRIRFVSDEYFSPGFCIHYNIVMPQFTEAVSPSVLPESA 180
Db 121 GRWCGSGTVPKGQISKGNIQIRIRFVSDEYFSPGFCIHYNIVMPQFTEAVSPSVLPESA 180
Qy 181 LPDLNNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
Db 181 LPDLNNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
Qy 241 LTEEVRVLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300
Db 241 LTEEVRVLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300
Qy 301 VTKKYHEVLQRPKTVGRGLHKSITDVALEHHEECDCVCRGSTGG 345
Db 301 VTKKYHEVLQRPKTVGRGLHKSITDVALEHHEECDCVCRGSTGG 345

RESULT 15
US-09-468-647A-103
; Sequence 103, Application US/09468647A
; Patent No. 6783953
; GENERAL INFORMATION:
; APPLICANT: Gordon, Robert D
; APPLICANT: Sprengel, Jorg J
; APPLICANT: Yon, Jeffery R
; APPLICANT: Dijkmans, Josiena J.H.
; APPLICANT: Gosiewska, Anna
; APPLICANT: Dhanaraj, Sri devi N
; APPLICANT: Xu, Jean
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-X

; FILE REFERENCE: B0192.70011US00
; CURRENT APPLICATION NUMBER: US/09/468,647A
; CURRENT FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: GB 9828377.3
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: US 60/124,967
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: US 60/164,131
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 103
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-468-647A-103

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 3, 2005, 19:21:57 ; Search time 109.5 Seconds
(without alignments)
1240.813 Million cell updates/sec

Title: US-09-818-943-1
 perfect score: 1858
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Gapop 10.0 , Gapext 0.5

Searched: 1774312 seqs, 393823214 residues

Total number of hits satisfying chosen parameters: 1774312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1858	100.0	345	9	US-09-618-943-1	Sequence 1, Appli
2	1858	100.0	345	9	US-09-852-209A-3	Sequence 3, Appli
3	1858	100.0	345	13	US-10-086-623-32	Sequence 32, App
4	1858	100.0	345	14	US-10-260-539-32	Sequence 32, App
5	1858	100.0	345	14	US-10-131-600-3	Sequence 3, Appl
6	1858	100.0	345	15	US-10-303-997B-3	Sequence 3, Appl
7	1858	100.0	345	15	US-10-439-337A-3	Sequence 3, Appl
8	1858	100.0	345	16	US-10-772-927A-7	Sequence 7, Appl
9	1851	99.6	345	9	US-09-823-033-2	Sequence 2, Appli
10	1851	99.6	345	9	US-09-923-095A-4	Sequence 4, Appli
11	1851	99.6	345	9	US-09-795-006A-149	Sequence 149, App

12	1851	99.6	345	9	US-09-978-295A-488	Sequence 488, App
13	1851	99.6	345	9	US-09-978-697-488	Sequence 488, App
14	1851	99.6	345	9	US-09-978-192A-488	Sequence 488, App
15	1851	99.6	345	9	US-09-999-832A-488	Sequence 488, App
16	1851	99.6	345	10	US-09-978-189-488	Sequence 488, App
17	1851	99.6	345	10	US-09-796-753-6	Sequence 6, Appli
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23	1851	99.6	345	10	US-09-999-831A-488	Sequence 488, App
24	1851	99.6	345	10	US-09-981-915A-488	Sequence 488, App
25	1851	99.6	345	10	US-09-978-824-488	Sequence 488, App
26	1851	99.6	345	10	US-09-918-585A-488	Sequence 488, App
27	1851	99.6	345	10	US-09-999-834A-488	Sequence 488, App
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43	1851	99.6	345	10	US-09-978-802A-488	Sequence 488, App
44	1851	99.6	345	11	US-09-876-813-33	Sequence 33, Appl
45	1851	99.6	345	11	US-09-999-831A-488	Sequence 488, App

ALIGNMENTS

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RESULT 1
US-09-818-943-1
; Sequence 1, Application US/09818943
; Patent No. US20020049987A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: Li, Xuri
; APPLICANT: FORTEN, Annica
; APPLICANT: AASE, Karin
; APPLICANT: Li, Hong
; TITLE OF INVENTION: NON-HUMAN TRAN
; FILE REFERENCE: 1064/48487
; CURRENT APPLICATION NUMBER: US/09/
; CURRENT FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/19
; PRIOR FILING DATE: 2000-03-28
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-818-943-1

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Query Match      100.0%; Score 1858; DB 9; Length 345;
Best Local Similarity 100.0%; Pred. No. 3..4e-174;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

US-09-852-209A-3
; Sequence 3, Application US/09852209A
; Patent No. US20020164687A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; APPLICANT: BETSHOLTZ, Christer
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING
; FILE REFERENCE: 09-410349-Eriksson et al-1064-44740
; CURRENT APPLICATION NUMBER: US/09/852,209A
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/410,349
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 60/110,749
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: 60/113,002
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 60/135,426
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 60/144,022
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-209A-3

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Best Local Similarity 100.0%; Pred. No. 3.4e-174;
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; Sequence 32, Application US/10086623
; Publication No. US20020164710A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: Li, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D, DNA CODING THEREFOR AND USES THEREOF
; FILE REFERENCE: 1064/44833C2
; CURRENT APPLICATION NUMBER: US/10/086,623
; CURRENT FILING DATE: 2000-03-04
; PRIOR APPLICATION NUMBER: US 60/107,852
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 60/113,997
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: US 60/150,604
; PRIOR FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: US 60/157,108
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: US 60/157,756
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 09/438,046
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 09/691,200
; PRIOR FILING DATE: 2000-10-19
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Amino acid sequence for PDGF-C
US-10-086-623-32

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; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LI, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET DERIVED GROWTH FACTOR D, DNA CODING THEREFOR AND USES TH
; FILE REFERENCE: 1064/44833C2
; CURRENT APPLICATION NUMBER: US/10/260,539
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US/10/086,623
; PRIOR FILING DATE: 2000-03-04
; PRIOR APPLICATION NUMBER: US 60/107,852
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 60/113,997
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: US 60/150,604
; PRIOR FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: US 60/157,108
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; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 09/438,046
; PRIOR FILING DATE: 1999-11-10
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; PRIOR FILING DATE: 2000-10-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Amino acid sequence for PDGF-C
US-10-260-539-32

Query Match 100.0%; Score 1858; DB 14; Length 345;
Best Local Similarity 100.0%; Pred. No. 3.4e-174;
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Qy 61 PRPHTYPRNTVLVWRLVAIVENWVQLTFDERFGLDEPDIDCKYDFVEVEEESDGTIL 120
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; Publication No. US20030082670A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; APPLICANT: BETHSHOLTZ, Christer
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING
; FILE REFERENCE: 09-410349-Eriksson et al-1064-44740
; CURRENT APPLICATION NUMBER: US/10/131,600
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US/09/410,349
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 60/108,109
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: 60/110,749
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: 60/113,002
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 60/135,426
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 60/144,022
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-131-600-3

Query Match 100.0%; Score 1858; DB 14; Length 345;
Best Local Similarity 100.0%; Pred. No. 3.4e-174;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MSLFGLLLVTSALAGQRRGTAESNLSSKQFSSNKQNGVQDPQHERIIITVSTNGSIHS 60
Db 1 MSLFGLLLVTSALAGQRRGTAESNLSSKQFSSNKQNGVQDPQHERIIITVSTNGSIHS 60
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; CURRENT FILING DATE: 2004-02-04
; PRIOR APPLICATION NUMBER: US 60/445,021
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: US 60/471,412
; PRIOR FILING DATE: 2003-05-16
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 7
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-772-927A-7

Query Match      100.0%; Score 1851; DB 16; Length 345;
Best Local Similarity 100.0%; Pred. No. 3.4e-174;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 PRPHTYPRNTVLVRLVAEENWVWVQLTDFRFGLEDPEDDICKYDFVEVEEPSDGTIL 120
QY 121 GRWCGSGTVPKGQISKGNQIRIRFVSDSEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPSPA 180
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QY 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
DB 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
QY 241 LEEVRLYSCPTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300
DB 241 LEEVRLYSCPTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300
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RESULT 9
US-09-823-033-2
; Sequence 2, Application US/09823033
; Patent No. US2002004225A1
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; FILE REFERENCE: 00-12
; CURRENT APPLICATION NUMBER: US/09/823,033
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-823-033-2

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Best Local Similarity 99.4%; Pred. No. 1.6e-173;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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DB 241 LEEVRLYSCPTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300
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DB 301 VTKYHEVLQRLPKTGVGRGLHKSITDVALEHHEECDCVCRGSTGG 345

RESULT 10
US-09-923-995-4
; Sequence 4, Application US/09923995
; Patent No. US20020081700A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: SNAKE VENOM POLYPEPTIDE ZSNK1
; FILE REFERENCE: 00-47
; CURRENT APPLICATION NUMBER: US/09/923,995
; CURRENT FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: US 60/223,164
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-923-995-4

Query Match      99.6%; Score 1851; DB 9; Length 345;
Best Local Similarity 99.4%; Pred. No. 1.6e-173;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY 121 GRWCGSGTVPKGQISKGNQIRIRFVSDSEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPSPA 180
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DB 301 VTKYHEVLQRLPKTGVGRGLHKSITDVALEHHEECDCVCRGSTGG 345

RESULT 11
US-05-795-006A-149
; Sequence 149, Application US/09795006A
; Patent No. US20020151860A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo et al
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; PRIOR APPLICATION NUMBER: 60/085704
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.6%; Score 1851; DB 9; Length 345;
Best Local Similarity 99.4%; Pred. No. 1.6e-173;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MSLFGLLIATVSALAGORGTQAESNLSSKFOFSSNKEQGVQDPQOHERIITVSTNGSIHS 60
Qy 61 PRFPHTYPRNTVLVRLVAVEENVWIIQLTDFERFGLDEPDDICKYDFVEVEEPSDGTIL 120
Db 61 PRFPHTYPRNTVLVRLVAVEENVWIIQLTDFERFGLDEPDDICKYDFVEVEEPSDGTIL 120
Qy 121 GRWCGSGTVPCKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPSPA 180
Db 121 GRWCGSGTVPCKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPSPA 180
Qy 181 LPDLNNAITAFSTLEDLIRYLEPERWQDLEDLIRPTWQLLGKAFVFGKRSRVVDLNL 240
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Qy 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300
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Qy 301 VTKKYHEVLQLRPKTGVRLHKSITDVALEHHBECDVCVRGSGTG 345
Db 301 VTKKYHEVLQLRPKTGVRLHKSITDVALEHHBECDVCVRGSGTG 345

RESULT 13
US-09-978-697-488
; Sequence 488, Application US/09978697
; Patent No. US20020169284A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC27
CURRENT APPLICATION NUMBER: US/09/978,697
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

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Query Match          99.6%; Score 1851; DB 9; Length 345;
Best Local Similarity 99.4%; Pred. No. 1.6e-173;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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US-09-978-192A-488
; Sequence 488, Application US/09978192A
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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
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; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
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; APPLICANT: Roy, Margaret Ann
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P3630P1C9
; CURRENT APPLICATION NUMBER: US/09/978,192A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
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; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078004
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079664
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079689

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Db 181 LFLDLNNAITAFSTLEDLRYLEPERWQLDEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
Qy 241 LTEEVRVLSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQVPSK 300
Db 241 LTEEVRVLSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQVPSK 300
Qy 301 VTKKYHEVLQRLPKTGVRGLHKLSTDLVALEHHEEDCDVCRGSTGG 345
Db 301 VTKKYHEVLQRLPKTGVRGLHKLSTDLVALEHHEEDCDVCRGSTGG 345

RESULT 15

US-09-999-832A-488
; Sequence 488, Application US/09999832A
; Publication No. US20020192706A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC63
; CURRENT APPLICATION NUMBER: US/09/999,832A
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
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; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
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; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078004
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20

; PRIOR APPLICATION NUMBER: 60/078936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078910
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; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079664
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; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079663
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; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/081070
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; PRIOR APPLICATION NUMBER: 60/081049
; PRIOR FILING DATE: 1998-04-08
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; PRIOR APPLICATION NUMBER: 60/081195
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081203
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081229
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081817
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081952
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081838
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082568
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082569
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082704
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082700
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082797

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 3, 2005, 19:08:39 ; Search time 118.5 Seconds
(without alignments)
1126.011 Million cell updates/sec

Title: US-09-818-943-2
Perfect score: 1848
Sequence: 1 MLLGLLLLTALAGRTGT.....DVALEHHBECDVCKGNAGG 345

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1848	100.0	345	3	Aay84559 A murine
2	1848	100.0	345	3	Aay96861 Murine va
3	1848	100.0	345	3	Aab48658 Mouse zve
4	1848	100.0	345	4	Aae00998 Mouse vge
5	1848	100.0	345	5	Abg92894 Mouse vge
6	1848	100.0	345	5	Aae13213 Mouse pla
7	1848	100.0	345	5	Aab47890 Mouse zve
8	1848	100.0	345	6	Abu72435 Mouse zve
9	1848	100.0	345	6	Abg76398 Mouse gro
10	1848	100.0	345	7	Adg47752 Mouse zve
11	1848	100.0	345	8	Adj32788 Mouse zve
12	1848	100.0	345	8	Adl18359 Mouse zve
13	1667	90.2	345	2	Aay41766 Human PRO
14	1667	90.2	345	2	Aay30023 Human vas
15	1667	90.2	345	2	Aay33679 Human vsg
16	1667	90.2	345	3	Aab33414 Human PRO
17	1667	90.2	345	3	Aab19578 Human PRO
18	1667	90.2	345	3	Aab10651 Human VEG
19	1667	90.2	345	3	Aab10633 Human RAC
20	1667	90.2	345	3	Aab10650 Human 990
21	1667	90.2	345	3	Aab10635 Human VEG
22	1667	90.2	345	3	Aab10644 Human VEG
23	1667	90.2	345	3	Aab44322 Human PRO
24	1667	90.2	345	3	Aab24412 Human PRO
25	1667	90.2	345	3	Aay59285 Bone morph

26	1667	90.2	345	3	Aay96858	Human gro
27	1667	90.2	345	3	Aab48657	Human zve
28	1667	90.2	345	3	Aab01419	Human TAN
29	1667	90.2	345	3	Aab24250	Human pla
30	1667	90.2	345	4	Aae02649	Human Lp8
31	1667	90.2	345	4	Aau12314	Human PRO
32	1667	90.2	345	4	Aab53074	Human ang
33	1667	90.2	345	4	Aab74028	Human VEG
34	1667	90.2	345	4	AAG65603	Human zve
35	1667	90.2	345	4	AAU08465	Polypepti
36	1667	90.2	345	4	AB50980	Human PRO
37	1667	90.2	345	4	AB49895	Human PRO
38	1667	90.2	345	4	AAE00997	Human zve
39	1667	90.2	345	5	ABB79984	Human vas
40	1667	90.2	345	5	ABG92889	Human VEG
41	1667	90.2	345	5	AB47889	Human zve
42	1667	90.2	345	5	ABB81331	Human VEG
43	1667	90.2	345	5	AAU76884	Human zve
44	1667	90.2	345	6	ABO17758	Novel hum
45	1667	90.2	345	6	ABU72434	Human zve

ALIGNMENTS

RESULT 1
AAY84559
ID AAY84559 standard; protein; 345 AA.
XX
AC AAY84559;
XX
DT 25-JUL-2000 (first entry)
XX
DE A murine platelet-derived growth factor C (PDGF-C).
XX
KW Platelet-derived growth factor C; PDGF-C; cell proliferation;
KW growth factor; heparin; connective tissue; wound healing; VEGF-F;
KW fibroblast mitogenesis; PDGF alpha receptor activation; tumour growth;
KW choriocarcinoma; Wilms tumour; megakaryoblastic leukaemia;
KW lung carcinoma; erythroleukemia; tissue remodelling.
XX
OS Mus sp.
XX
PN WO200018212-A2.
XX
PD 06-APR-2000.
XX
PF 30-SEP-1999; 99WO-US022668.
XX
PR 30-SEP-1998; 98US-0102461P.
PR 12-NOV-1998; 98US-0108109P.
PR 03-DEC-1998; 98US-0110749P.
PR 18-DEC-1998; 98US-0113002P.
PR 21-MAY-1999; 99US-0135426P.
PR 15-JUL-1999; 99US-0144022P.
XX
(LUDW-) LUDWIG INST CANCER RES.
XX
(UYHE-) UNIV HELSINKI LICENSING LTD.
PA
Eriksson U, Aase K, Lee X, Ponten A, Untela M, Alitalo K;
PI Oestman A, Heldin C, Betsholz C;
XX
WPI; 2000-292954/25.
DR N-PSDB; AAA12525.
XX
PT Novel DNA encoding PDGF-C useful to stimulate or enhance proliferation,
PT differentiation, growth and motility of cells expressing the PDGF-C
PS receptor.
XX
PS Claim 27; Fig 6; 135pp; English.
XX
CC The present sequence represents murine platelet-derived growth factor C
(PDGF-C) (formally designated VEGF-F). PDGF-C polypeptides have the

CC ability to stimulate and enhance proliferation or differentiation, and/or
CC growth or motility of cells expressing a PDGF-C receptor. PDGF-C
CC polypeptides can be used in pharmaceuticals for promoting cell
CC proliferation, preferably in combination with one other growth factor and
CC heparin. Pharmaceuticals comprising PDGF-C polypeptides can also be used
CC for stimulating connective tissue or wound healing. The PDGF-C
CC polypeptide can be enzymatically processed to generate the active
CC truncated form of PDGF-C and used to regulate the receptor-binding
CC specificity of PDGF-C. PDGF-C can also be used to promote fibroblast
CC mitogenesis in a mammal and to induce PDGF alpha receptor activation.
CC PDGF-C antagonists can be used to inhibit tumour growth of a tumour
CC expressing PDGF-C in a mammal. Specific types of human tumours, e.g.
CC choriocarcinoma, Wilms tumour, megakaryoblastic leukaemia, lung carcinoma
CC and erythroleukemia, can be identified by testing for expression of PDGF-
CC C. PDGF-C antagonists can also be used to inhibit tissue remodeling
CC during invasion of tumour cells into a normal population of cells.
CC Antagonists can also be used to treat fibrotic conditions, especially
CC found in the lung, kidney or liver

XX Sequence 345 AA;

Query Match 100.0%; Score 1848; DB 3; Length 345;
Best Local Similarity 100.0%; Pred. No. 3e-181;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGLLLLTSAAGQRTGTRAESNLSSKQLQSSDKQNGVQDPHRRVVTISNGSIHS 60
DB 1 MLLGLLLLTSAAGQRTGTRAESNLSSKQLQSSDKQNGVQDPHRRVVTISNGSIHS 60
QY 61 PKFPHYPRNMVWRLVAVDENVRITQTFDERFGLDEPDDEICKYDFVEVEPSDGSVL 120
DB 61 PKFPHYPRNMVWRLVAVDENVRITQTFDERFGLDEPDDEICKYDFVEVEPSDGSVL 120
QY 121 GRWCGSGTVPGKQTSKGNHIRFVSDYFPEPFCIHYSIIMQVTTTSPSLPSS 180
DB 121 GRWCGSGTVPGKQTSKGNHIRFVSDYFPEPFCIHYSIIMQVTTTSPSLPSS 180
QY 181 LSLDLLNNAVTAFSTLEELIRYLEPRQWVDLSLYKPTWQLLKAFYKSKSVNNL 240
DB 181 LSLDLLNNAVTAFSTLEELIRYLEPRQWVDLSLYKPTWQLLKAFYKSKSVNNL 240
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNCCVPRK 300
DB 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNCCVPRK 300
QY 301 VTKKYHEVLQRPKTVGKGLHKSLLTDVALEHHEECDCVCRNAGG 345
DB 301 VTKKYHEVLQRPKTVGKGLHKSLLTDVALEHHEECDCVCRNAGG 345

RESULT 2
AAY96861
ID AAY96861 standard; protein; 345 AA.

AC AAY96861;
XX 26-SEP-2000 (first entry)
XX Murine vascular endothelial growth factor homologue, ZVEGF3.
XX Vascular endothelial growth factor; homologue; zveg3; CUB domain;
KW Cysteine knot; platelet-derived growth factor; PDGF; neuropilin;
KW Chromosome 4q28.3; cytostatic; anti-psoriatic; anti-inflammatory;
KW anti-diabetic; ophthalmological; anti-rheumatic; anti-arthritis;
vulnerary.
XX Mus musculus.
XX WO200034474-A2.
XX 15-JUN-2000.
XX 07-DEC-1999; 99WO-US028968.

XX 07-DEC-1998; 98US-00207120.
PR 06-JUL-1999; 99US-0142578P.
PR 21-OCT-1999; 99US-0161653P.
PR 12-NOV-1999; 99US-0165255P.
PA (ZYMO) ZYMOGENETICS INC.
XX Gao Z, Hart CE, Piddington CS, Sheppard PO, Shoemaker KE;
PI Gilbertson DG, West JW;
XX WPI; 2000-423420/36.
DR N-PSDB; AAA51527.
XX Novel zveg3 polypeptides and nucleotides encoding them useful for
PT stimulating growth of smooth muscle cells and fibroblasts comprising an
PT epitope bearing portion of a specific amino acid sequence.
XX Claim 1; Page 169-170; 173pp; English.

XX This shows a murine ZVEGF3 a novel vascular endothelial growth factor
CC homologue. Polypeptides comprising an epitope-bearing portion human or
CC murine ZVEGF3 are claimed. The growth factors comprise a growth factor
CC domain and a CUB domain (generic sequence motifs are shown in AAY96859
CC and AAY96860). The growth factor domain is characterized by an
CC arrangement of cysteine residues and beta-strands that is characteristic
CC of the "cysteine knot" structure of the platelet-derived growth factor
CC (PDGF) family. The CUB domain shows homology to CUB domains in
CC neuropilins, human bone morphogenetic protein-1, porcine seminal plasma
CC protein, bovine acidic seminal fluid protein and Xenopus laevis tollid-
CC like protein. Structural analysis and homology predict that ZVEGF3
CC polypeptides complex with a second polypeptide to form multimeric
CC proteins. The human zveg3 gene has been mapped to chromosome 4q28.3.
CC ZVEGF3 is useful for stimulating the growth of fibroblasts or smooth
CC muscle cells, for activating cell surface PDGF-alpha receptor and for
CC inhibiting PDGF-alpha receptor mediated cellular processes. ZVEGF3 is
CC useful for regulating (post-development) organ growth, regeneration and
CC maintenance, as well as tissue maintenance and repair processes. ZVEGF3
CC antagonists are useful for treating cancer, rheumatoid arthritis, disease,
CC diabetic retinopathy, ischemic limb disease, peripheral vascular disease,
CC myocardial ischemia, vascular intimal hyperplasia, atherosclerosis, wound
CC healing, chronic liver disease and haemangioma formation. ZVEGF3 can also
CC be used to modulate neurite growth and development of the nervous system,
CC and for treating neurodegenerative diseases

XX Sequence 345 AA;

Query Match 100.0%; Score 1848; DB 3; Length 345;
Best Local Similarity 100.0%; Pred. No. 3e-181;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGLLLLTSAAGQRTGTRAESNLSSKQLQSSDKQNGVQDPHRRVVTISNGSIHS 60
DB 1 MLLGLLLLTSAAGQRTGTRAESNLSSKQLQSSDKQNGVQDPHRRVVTISNGSIHS 60
QY 61 PKFPHYPRNMVWRLVAVDENVRITQTFDERFGLDEPDDEICKYDFVEVEPSDGSVL 120
DB 61 PKFPHYPRNMVWRLVAVDENVRITQTFDERFGLDEPDDEICKYDFVEVEPSDGSVL 120
QY 121 GRWCGSGTVPGKQTSKGNHIRFVSDYFPEPFCIHYSIIMQVTTTSPSLPSS 180
DB 121 GRWCGSGTVPGKQTSKGNHIRFVSDYFPEPFCIHYSIIMQVTTTSPSLPSS 180
QY 181 LSLDLLNNAVTAFSTLEELIRYLEPRQWVDLSLYKPTWQLLKAFYKSKSVNNL 240
DB 181 LSLDLLNNAVTAFSTLEELIRYLEPRQWVDLSLYKPTWQLLKAFYKSKSVNNL 240
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNCCVPRK 300
DB 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNCCVPRK 300
QY 301 VTKKYHEVLQRPKTVGKGLHKSLLTDVALEHHEECDCVCRNAGG 345

Db 301 VTKKYHEVLQRLPKTVGKGLHKSLTDVALEHHEBCDCVCRNAGG 345

RESULT 3

ID AAB48658 standard; protein; 345 AA.

AC AAB48658;

DT 09-MAR-2001 (first entry)

DE Mouse zveg3, SEQ ID NO:35.

KW Mouse; zveg3; zveg4 fusion; growth factor homologue; VEGF/PDGF family; murine; CUB domain; PDGF-like activity; mitogenic; osteogenic; neovascularisation; tissue repair; proliferation; differentiation; liver damage; neurodegenerative; Alzheimer's disease; multiple sclerosis; periodontal disease; bone fracture; wound healing; vulnery; ischaemia; immunomodulation; hepatic.

XX Mus musculus.

OS WO200066736-A1.

PN 09-NOV-2000.

PD 03-MAY-2000; 2000WO-US040047.

PR 03-MAY-1999; 99US-00304216.

PR 10-NOV-1999; 99US-0164463P.

PR 04-FEB-2000; 2000US-01801699.

XX (ZYMO) ZYMOGENETICS INC.

PI Gilbert T, Hart CE, Sheppard PO, Gilbertson DG;

XX WPI; 2000-687541/67.

DR N-PSDB; AAC81583.

XX Growth factor homologs and the nucleic acids that encode them, useful e.g. for treating liver damage, ischemia, multiple sclerosis and Alzheimer's disease.

PS Disclosure; Page 130-131; 143pp; English.

XX The invention relates to the human growth factor homologue zveg4 (AAB48653), and nucleic acids encoding it (AAC81583). Zveg4 is a member of the PDGF (platelet-derived growth factor)/VEGF (vascular endothelial growth factor) family. Zveg4 has a growth factor domain (AAB48654) characterised by a PDGF cysteine knot structure, and a CUB domain (AAB48655) which has a beta barrel structure. Zveg4 has PDGF-like activity, having mitogenic activity on fibroblasts, vascular smooth muscle cells and pericytes, and has also been shown to stimulate bone growth. The invention also relates to fusion proteins comprising human zveg4 or fragments thereof, particularly human zveg4/human zveg3 fusions; expression constructs and host cells comprising human zveg4 nucleic acids; the recombinant expression of human zveg4; an antibody which binds to human zveg4 or a fragment thereof; a method of activating a cell-surface PDGF receptor using a zveg4-derived polypeptide; a method of modulating the proliferation, differentiation, migration or metabolism of bone cells, comprising exposing bone cells to zveg4-derived polypeptides; and a method of detecting a genetic abnormality in the zveg4 gene of a patient. Zveg4 proteins and derived fragments may be used to stimulate tissue development or repair, or cellular differentiation or proliferation. They are particularly used for the treatment or repair of liver damage, and may also be used to modulate neurite growth (e.g., in the treatment of Alzheimer's disease or multiple sclerosis). Due to their osteogenic activity, they may be used in the treatment of periodontal disease and fractures. They may also be used to enhance expansion and mobilisation of haematopoietic stem cells and endothelial precursor stem cells, which may be useful in the treatment of ischaemia, in wound healing, and in the modulation of the immune system. The present sequence represents mouse zveg3

XX SQ

Sequence 345 AA;

Query Match 100.0%; Score 1848; DB 3; Length 345;
Best Local Similarity 100.0%; Pred. No. 3e-181;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLTSALAGQRTGTRAESNLSSKLQSSDKEQGVQDPRHRRVVTISNGSIHS 60

Db 1 MLLGLLLTSALAGQRTGTRAESNLSSKLQSSDKEQGVQDPRHRRVVTISNGSIHS 60

QY 61 PKPHTYPRNNVWLVAVDENVRIQLTFDERGLEDPDDICKYDFVEEPEPSDGSVL 120

Db 61 PKPHTYPRNNVWLVAVDENVRIQLTFDERGLEDPDDICKYDFVEEPEPSDGSVL 120

QY 121 GRWCSGTVPGKQTSKGNHIRFVSDRYFFSEPGFCIHYSIIMPOVTETTSVLPSS 180

Db 121 GRWCSGTVPGKQTSKGNHIRFVSDRYFFSEPGFCIHYSIIMPOVTETTSVLPSS 180

QY 181 LSLDLNNAVTAFTLEELIRYLPDRMQVDLSLYKFTWQLLKAFYKSKSVNVLNL 240

Db 181 LSLDLNNAVTAFTLEELIRYLPDRMQVDLSLYKFTWQLLKAFYKSKSVNVLNL 240

QY 241 LKEEVKLYSCTPRNFSVSIIRBELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300

Db 241 LKEEVKLYSCTPRNFSVSIIRBELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300

QY 301 VTKKYHEVLQRLPKTVGKGLHKSLTDVALEHHEBCDCVCRNAGG 345

Db 301 VTKKYHEVLQRLPKTVGKGLHKSLTDVALEHHEBCDCVCRNAGG 345

RESULT 4

AAE00998

ID AAE00998 standard; protein; 345 AA.

XX AC AAE00998;

DT 04-JUL-2001 (first entry)

DE Mouse zveg3 protein.

XX Mouse; Zveg3 antagonist; cell proliferation; stellate cell activation; extracellular matrix production; fibrosis; VEGF-R; PDGF-C;
KW platelet-derived growth factor; PDGF; vascular endothelial growth factor;
KW VEGF; mitogenic effect; therapy; keloid; scleroderma; fibrotic disorder;
KW chronic active hepatitis; fulminant viral hepatitis; amyloidosis;
KW diabetic nephropathy; alpha-1-antitrypsin deficiency; silicosis;
KW asbestosis; renal arteriosclerosis; post necrotic cirrhosis;
KW diabetic glomerulosclerosis; focal glomerulosclerosis; hyperostosis;
KW pulmonary hypertension; idiopathic pulmonary fibrosis; osteopetrosis;
KW bronchiolitis obliterans-organising pneumonia; transplant vasculopathy;
KW fibroproliferative disorder.

XX Mus musculus.

XX WO200128586-A1.

PD 26-APR-2001.

XX 23-OCT-2000; 2000WO-US029270.

XX 21-OCT-1999; 99US-0161653P.

PR 12-NOV-1999; 99US-0165255P.

PR 01-AUG-2000; 2000US-022223P.

XX (ZYMO) ZYMOGENETICS INC.

PI Gilbertson DG;

XX WPI; 2001-300278/31.

DR N-PSDB; AAD04650.

XX

PT Use of zvegf3 antagonist for reducing fibroproliferative disorder of
PT kidney, liver and bone, reducing extracellular matrix production,
PT treating fibrosis or reducing stellate cell activation in mammal.
XX Example 2; Fig 2; 70pp; English.

XX The patent discloses materials and methods for reducing cell
CC proliferation or extracellular matrix production, treating fibrosis and
CC reducing stellate cell activation in a mammal. The method comprises
CC administering a composition containing a zvegf3 antagonist in combination
CC with a delivery vehicle. The zvegf3 is a protein that is structurally
CC related to platelet-derived growth factor (PDGF) and the vascular
CC endothelial growth factors (VEGF). The zvegf3 protein is also designated
CC as "VEGF-R" and "PDGF-C". The zvegf3 antagonist is useful to block the
CC mitogenic effects of zvegf3 and thereby to inhibit or prevent and treat
CC keloids, scleroderma, fibrotic disorders of liver such as chronic active
CC hepatitis, fulminant viral hepatitis, post necrotic cirrhosis and alpha-1
CC -antitrypsin deficiency, fibrotic disorders of the kidney such as
CC diabetic glomerulosclerosis, focal glomerulosclerosis, diabetic
CC nephropathy, amyloidosis and renal arteriosclerosis, fibrotic disorders
CC of the lung such as silicosis, asbestosis, idiopathic pulmonary fibrosis,
CC bronchitis obliterans, organising pneumonia and pulmonary hypertension,
CC fibrotic disorders of pancreas, fibroproliferative disorders of the
CC vasculature such as transplant vasculopathy and fibroproliferative
CC disorders of the bone such as osteopetrosis and hyperostosis. The present
CC sequence is mouse zvegf3 protein

XX Sequence 345 AA;

- Query Match 100.0%; Score 1848; DB 4; Length 345;
Best Local Similarity 100.0%; Pred. No. 3e-181;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLTSLAGQRTTAEENLSSKQLSSDKQNGVQDPHRRVVTISGNGSIHS 60
Db 1 MLLGLLLTSLAGQRTTAEENLSSKQLSSDKQNGVQDPHRRVVTISGNGSIHS 60
QY 61 PKFPHYTPNNVLWRLVAVDENVRQLTDFRFGLEDDEDDICKYDFVEEPESDGVL 120
Db 61 PKFPHYTPNNVLWRLVAVDENVRQLTDFRFGLEDDEDDICKYDFVEEPESDGVL 120
QY 121 GRWCGSGTVPKGQTSKGNHIRFVSDEYFPSEPGFCIHYSIIMQVTTTSPSLPSS 180
Db 121 GRWCGSGTVPKGQTSKGNHIRFVSDEYFPSEPGFCIHYSIIMQVTTTSPSLPSS 180
QY 181 LSLDLLNNAVTAFTLEELIRYLEPDRWQVLDLSLYKPTWQLLGAFLYKKSQVNNL 240
Db 181 LSLDLLNNAVTAFTLEELIRYLEPDRWQVLDLSLYKPTWQLLGAFLYKKSQVNNL 240
QY 241 LKEEVKLYSCTPRNFSVSIRELKRDTTFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
Db 241 LKEEVKLYSCTPRNFSVSIRELKRDTTFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
QY 301 VTKYKHEVLQRPKTVGKGLHSLTDVALEHHEEDCDVCGRNAGG 345
Db 301 VTKYKHEVLQRPKTVGKGLHSLTDVALEHHEEDCDVCGRNAGG 345

RESULT 5
ABG92894

ID ABG92894 standard; protein; 345 AA.

XX AC ABG92894;

XX 19-NOV-2002 (first entry)

XX Mouse VEGF-like protein zvegf 3.

XX VEGF; vascular endothelial growth factor; zvegf 3; mouse; chromosome 3;
KW cell proliferation; differentiation; metabolism; migration;
KW revascularisation; solid tumour; diabetic retinopathy; psoriasis;
KW rheumatoid arthritis; cancer; autoimmune disease; inflammation;
KW myocardial ischaemia; scleroderma; fibrosis; glomerulosclerosis;

KW atherosclerosis; skin wound; ulcer; burn; skin grafting;
KW female reproductive tract disorder; chronic liver disease;
KW circulatory disorder; heart failure; neurodegenerative disease;
KW multiple sclerosis; Parkinson's disease; Alzheimer's disease; stroke;
KW neurite outgrowth.
XX Mus musculus.
OS US6432673-B1.
XX 13-AUG-2002.
XX 07-DEC-1999; 99US-00457066.
XX 07-DEC-1998; 98US-011173P.
PR 06-JUL-1999; 99US-0142576P.
PR 21-OCT-1999; 99US-0161653P.
PR 12-NOV-1999; 99US-0165255P.
XX (ZYMO) ZYMOGENETICS INC.
PA Gao Z, Hart CE, Piddington CS, Sheppard PO, Shoemaker KE;
PI Gilbertson DG, West JW;
XX WPI: 2002-689759/74.
DR N-PSDB; ABS68648.
XX Novel polypeptide, designated zvegf3 useful for treating skin wounds,
PT ulcers, burns, skin grafting, female reproductive tract disorders,
PT Parkinson's disease, and Alzheimer's disease.
XX Example 4; Fig 2; 68pp; English.

CC The invention relates to an isolated polypeptide, designated zvegf3 (a
CC vascular endothelial growth factor-like protein) of 111-136 amino acid
CC residues in length and comprises the sequence appearing as ABG92889 from
CC amino acid residues 235-345. Also included are an isolated protein
CC comprising a first polypeptide disulphide bonded to a second polypeptide,
CC where each of the first and second polypeptides is from zvegf 3, and
CC where the protein modulates cell proliferation, differentiation,
CC metabolism or migration, the zvegf 3 encoding polynucleotides and zvegf 3
CC expression vectors and host cells. Zvegf 3 is useful as additives in
CC tissue adhesives for promoting revascularisation of the healing tissue,
CC for designing molecules that antagonise semaphorin-stimulated activities,
CC including neurite growth, cardiovascular development, cartilage and limb
CC development, and T and B-cell function, and for imaging tumours or other
CC sites of abnormal cell proliferation and in gene therapy applications.
CC The proteins are useful therapeutically to stimulate tissue development
CC or repair, or cellular differentiation or proliferation, for stimulating
CC the growth of fibroblast or smooth muscle cells, as molecular weight
CC standards, as reagents in assays for determining circulatory level of the
CC protein or as standards in the analysis of cell phenotype, for reducing
CC identifying inhibitors of their activity which are useful for reducing
CC the growth of solid tumours, for treating diabetic retinopathy,
CC psoriasis, rheumatoid arthritis, various forms of cancers, autoimmune
CC disease, inflammation, myocardial ischaemia, scleroderma, and reducing
CC fibrosis, including scar formation, keloids, liver fibrosis, lung
CC fibrosis (e.g. silicosis, asbestosis), kidney fibrosis (including
CC diabetic nephropathy), glomerulosclerosis, atherosclerosis, skin wounds,
CC ulcers, burns, skin grafting, and female reproductive tract disorders,
CC chronic liver disease (hepatitis), cirrhosis, Reye's syndrome, Wilson's
CC disease, circulatory disorders e.g. heart failure, hepatic or portal vein
CC thrombosis, cardiac sclerosis, neurodegenerative diseases such as
CC multiple sclerosis, Parkinson's disease, Alzheimer's disease, and for
CC regenerating neurite outgrowths following strokes. The gene for mouse
CC zvegf3 is located on chromosome 3. The present sequence represents zvegf
CC 3

SQ Sequence 345 AA;

Query Match 100.0%; Score 1848; DB 5; Length 345;
Best Local Similarity 100.0%; Pred. No. 3e-181;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLLTALAGQRTGTRAESNLSSKLQSSDKEQNGVQDPRHERVVTISGNGSIHS 60
DB 1 MLLGLLLLTALAGQRTGTRAESNLSSKLQSSDKEQNGVQDPRHERVVTISGNGSIHS 60
QY 61 PKFPHYPRNMVLRVAVDENVRILQTFDERFGLDEPDDICKYDFVEVEEPPSDGVL 120
DB 61 PKFPHYPRNMVLRVAVDENVRILQTFDERFGLDEPDDICKYDFVEVEEPPSDGVL 120
QY 121 GRWCSGTVPGKQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMQVTTTSPSLPSS 180
DB 121 GRWCSGTVPGKQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMQVTTTSPSLPSS 180
QY 181 LSLLDNNAVTAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLLGAFLYGGKSKVVNLNL 240
DB 181 LSLLDNNAVTAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLLGAFLYGGKSKVVNLNL 240
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
DB 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
QY 301 VTKKYHEVLQRLPKTGKGLHSLTDVALEHHEECDCVCRGNAGG 345
DB 301 VTKKYHEVLQRLPKTGKGLHSLTDVALEHHEECDCVCRGNAGG 345

RESULT 6
AAE13213
ID AAE13213 standard; protein; 345 AA.
XX AAE13213;
AC AAE13213;
DT 12-FEB-2002 (first entry)
DE Mouse platelet-derived growth factor (PDGF-C) protein.
XX Mouse; transgenic animal; platelet derived growth factor C; PDGF-C;
KW cardiac hypertrophy; fibrosis.
XX Mus sp.
XX WO200172132-A1.
XX 04-OCT-2001.
XX 28-MAR-2001; 2001WO-US009855.
XX 28-MAR-2000; 2000US-0192507P.
XX (LUDW-) LUDWIG INST CANCER RES.
XX Eriksson U, Li X, Ponten A, Aase K, Li H;
XX WPI; 2002-010700/01.
XX A transgenic animal over-expressing platelet derived growth factor C is
XX useful to study and find therapy for disease associated with PDGF-C over-
XX expression, including cardiac hypertrophy and fibrosis.
XX Example 4; Page 42-43; 48pp; English.
XX The patent discloses a method for producing a transgenic, non-human
XX animal over-expressing a platelet derived growth factor C (PDGF-C), or
XX its functional fragment or analogue. The method involves introducing a
XX transgenic PDGF-C DNA into a cell of a non-human animal, introducing the
XX cell into a non-human animal and allowing the cell to develop into a
XX transgenic, non-human animal. The transgenic animal is useful as a model
XX to study disease states characterised by over-expression of PDGF-C and to
XX find therapy for those diseases, particularly hypertrophy and fibrosis in
XX various organs including the heart. The present sequence is PDGF-C
XX protein from mouse
XX Sequence 345 AA;
SQ

Query Match 100.0%; Score 1848; DB 5; Length 345;
Best Local Similarity 100.0%; Pred. No. 3e-181;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGLLLLTALAGQRTGTRAESNLSSKLQSSDKEQNGVQDPRHERVVTISGNGSIHS 60
DB 1 MLLGLLLLTALAGQRTGTRAESNLSSKLQSSDKEQNGVQDPRHERVVTISGNGSIHS 60
QY 61 PKFPHYPRNMVLRVAVDENVRILQTFDERFGLDEPDDICKYDFVEVEEPPSDGVL 120
DB 61 PKFPHYPRNMVLRVAVDENVRILQTFDERFGLDEPDDICKYDFVEVEEPPSDGVL 120
QY 121 GRWCSGTVPGKQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMQVTTTSPSLPSS 180
DB 121 GRWCSGTVPGKQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMQVTTTSPSLPSS 180
QY 181 LSLLDNNAVTAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLLGAFLYGGKSKVVNLNL 240
DB 181 LSLLDNNAVTAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLLGAFLYGGKSKVVNLNL 240
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
DB 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
QY 301 VTKKYHEVLQRLPKTGKGLHSLTDVALEHHEECDCVCRGNAGG 345
DB 301 VTKKYHEVLQRLPKTGKGLHSLTDVALEHHEECDCVCRGNAGG 345
RESULT 7
AAE47890
ID AAE47890 standard; protein; 345 AA.
XX AAE47890;
AC AAE47890;
DT 16-MAY-2002 (first entry)
DE Mouse zveg3.
XX Human; mouse; zveg3; zveg4; platelet derived growth factor; PDGF;
KW homolog; growth; bone; ligament; cartilage; proliferation; osteoblast;
KW chondrocyte; bony defect; fracture; bone graft; implant;
KW periodontal pocket; osteoclast; bone marrow stem cell; osteoporosis.
XX Mus musculus.
XX US2002004225-A1.
XX 10-JAN-2002.
XX 29-MAR-2001; 2001US-00823033.
XX 07-DEC-1998; 98US-0111173P.
XX 06-JUL-1999; 99US-0142576P.
XX 21-OCT-1999; 99US-0161653P.
XX 12-NOV-1999; 99US-0165255P.
XX 07-DEC-1999; 99US-00457066.
XX 31-MAR-2000; 2000US-0193723P.
XX (HART/) HART C E.
XX (GILB/) GILBERTSON D G.
XX Hart CE, Gilbertson DG;
XX WPI; 2002-171026/22.
XX N-PSDB; AA172444.
XX Promoting growth of bone, ligament or cartilage in a mammal, involves
XX administering to the mammal a protein which comprises growth factor
XX domain of zveg3 protein, a homolog of platelet-derived growth factor.
XX Claim 1; Page 19-20; 31pp; English.
PS

XX The sequences given in AAB47889-90 represent human and mouse zvegfg3,
CC respectively. zvegfg3 is a platelet derived growth factor (PDGF) homolog
CC and it was used in the method of the invention for promoting growth of
CC bone, ligament or cartilage and stimulating proliferation of osteoblasts
CC or chondrocytes in a mammal. The proteins used were preferably a dimeric
CC protein of residues 235-345 of human zvegfg3 or all of the mouse zvegfg3
CC protein, with a delivery vehicle. The method of th invention is useful
CC for promoting growth of bone, ligament or cartilage in a mammal, where
CC the composition is administered at a site of a bony defect, preferably a
CC fracture, bone graft site, implant site, or periodontal pocket, and for
CC stimulating proliferation of osteoblasts or chondrocytes in a mammal. It
CC is further useful for promoting proliferation of osteoblasts.
CC osteoclasts, chondrocytes or bone marrow stem cells, where the bone
CC marrow stem cells are harvested from a patient prior to culture. The
CC method is therefore useful for treating osteoporosis
XX
SQ Sequence 345 AA;

Query Match 100.0%; Score 1848; DB 5; Length 345;
Best Local Similarity 100.0%; Pred. No. 3e-181;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGLLLLTALAGQRTGTRAESNLSSKQLQSSDKQNGVQDPHERVVTISNGSGTHS 60
DB 1 MLLGLLLLTALAGQRTGTRAESNLSSKQLQSSDKQNGVQDPHERVVTISNGSGTHS 60
QY 61 PKFPHYPRNMVLMVRLVAVDENVRIOQLTDFERFGLDEPDIDCKYDFVEEPEPSDGSVL 120
DB 61 PKFPHYPRNMVLMVRLVAVDENVRIOQLTDFERFGLDEPDIDCKYDFVEEPEPSDGSVL 120
QY 121 GRWCSTGTPGKQTSKGNHIRFVSDYFPSEPGFCIHYSIIMPQVTTTSPSLPSS 180
DB 121 GRWCSTGTPGKQTSKGNHIRFVSDYFPSEPGFCIHYSIIMPQVTTTSPSLPSS 180
QY 181 LSLDLLNNAVTAFSTLEELIRYLPDRQVLDLSYKPTWQLLKAFYLGKSKVNNLNL 240
DB 181 LSLDLLNNAVTAFSTLEELIRYLPDRQVLDLSYKPTWQLLKAFYLGKSKVNNLNL 240
QY 241 LKEEVKLYSCTPRNFSVSIRELKRDTITFWPGCLLVKRCGNCACCLHNCNECCVPRK 300
DB 241 LKEEVKLYSCTPRNFSVSIRELKRDTITFWPGCLLVKRCGNCACCLHNCNECCVPRK 300
QY 301 VTKKYHEVLQLRPKTGVKGLHSLTDVALEHHEECDCVCRNAGG 345
DB 301 VTKKYHEVLQLRPKTGVKGLHSLTDVALEHHEECDCVCRNAGG 345

RESULT 8
ABU72435
ID ABU72435 standard; protein; 345 AA.

XX AC ABU72435;
XX
DT 16-JUN-2003 (first entry)
XX
DE Mouse ZVEGF4-related protein #1.
XX
KW Growth factor homologue; ZVEGF4; proliferation; differentiation;
KW migration; mesenchymal cell; cell surface semaphorin; neuropilin;
KW neurite growth; cardiovascular development; limb development;
KW cartilage development; T-cell; B-cell; rheumatoid arthritis; cancer;
KW autoimmune disease; inflammation; retinopathy; haemangioma;
KW ischaemic event; neuropathy; acute nerve damage; stroke;
KW central nervous system disease; peripheral nervous system disease.
XX
OS Mus musculus.
XX
PN US6495668-B1.
XX
PD 17-DEC-2002.
XX
PF 03-MAY-2000; 2000US-00564595.

XX 03-MAY-1999; 99US-0132250P.
PR 10-NOV-1999; 99US-0184463P.
PR 04-FEB-2000; 2000US-0180169P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Gilbert T, Hart CE, Sheppard PO, Gilbertson DG;
XX
XX WPI; 2003-352153/33.
DR N-PSDB; ACA64137.
XX
XX Isolated growth factor analogue ZVEGF4 proteins for pharmaceutical
PT composition as, e.g. therapeutic agents, diagnostic agents, and research
PT tools and reagents, includes polypeptides from amino acid residues.
XX
PS Disclosure; Col 95-98; 67pp; English.
XX

CC The invention relates to an isolated protein comprising a first
CC polypeptide disulphide-bonded to a second polypeptide. The first and
CC second polypeptides are from 113-138 amino acid residues and comprises
CC 258-370 amino acid residues of human growth factor homologue ZVEGF4. The
CC protein stimulates proliferation, differentiation, or migration of
CC mesenchymal cells and may modulate activities mediated by cell surface
CC semaphorins. ZVEGF4 may be used to design ant/agonists of neuropilin-
CC semaphorin interactions which may be of use in neurite growth,
CC cardiovascular development, cartilage and limb development, T- and B-cell
CC functions as well as treating rheumatoid arthritis, various forms of
CC cancer, autoimmune diseases, inflammation, retinopathies, haemangiomas,
CC ischaemic events, neuropathies, acute nerve damage, central nervous
CC system diseases and peripheral nervous system diseases including stroke.
CC The isolated protein is also used for a pharmaceutical composition as
CC therapeutic agents, diagnostic agents, and research tools and reagents.
CC It can be used in the study and regulation of cell and tissue
CC development, as components of cell culture media. The proteins can form
CC homodimers or heterodimers that act on tissues to control organ
CC development by modulating cell proliferation, migration, differentiation,
CC or metabolism. The gene for human ZVEGF4 is located on chromosome 11q22.3
CC -23.1. A transgene construct was made for producing mice transgenic for
CC human ZVEGF4. The construct contained human growth hormone gene control
CC regions. The present sequence is a ZVEGF4-related protein sequence. Note:
CC The present sequence is included in the sequence listing but is not
CC mention elsewhere in the specification
XX

SQ Sequence 345 AA;

Query Match 100.0%; Score 1848; DB 6; Length 345;
Best Local Similarity 100.0%; Pred. No. 3e-181;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLLTALAGQRTGTRAESNLSSKQLQSSDKQNGVQDPHERVVTISNGSGTHS 60
DB 1 MLLGLLLLTALAGQRTGTRAESNLSSKQLQSSDKQNGVQDPHERVVTISNGSGTHS 60
QY 61 PKFPHYPRNMVLMVRLVAVDENVRIOQLTDFERFGLDEPDIDCKYDFVEEPEPSDGSVL 120
DB 61 PKFPHYPRNMVLMVRLVAVDENVRIOQLTDFERFGLDEPDIDCKYDFVEEPEPSDGSVL 120
QY 121 GRWCSTGTPGKQTSKGNHIRFVSDYFPSEPGFCIHYSIIMPQVTTTSPSLPSS 180
DB 121 GRWCSTGTPGKQTSKGNHIRFVSDYFPSEPGFCIHYSIIMPQVTTTSPSLPSS 180
QY 181 LSLDLLNNAVTAFSTLEELIRYLPDRQVLDLSYKPTWQLLKAFYLGKSKVNNLNL 240
DB 181 LSLDLLNNAVTAFSTLEELIRYLPDRQVLDLSYKPTWQLLKAFYLGKSKVNNLNL 240
QY 241 LKEEVKLYSCTPRNFSVSIRELKRDTITFWPGCLLVKRCGNCACCLHNCNECCVPRK 300
DB 241 LKEEVKLYSCTPRNFSVSIRELKRDTITFWPGCLLVKRCGNCACCLHNCNECCVPRK 300
QY 301 VTKKYHEVLQLRPKTGVKGLHSLTDVALEHHEECDCVCRNAGG 345
DB 301 VTKKYHEVLQLRPKTGVKGLHSLTDVALEHHEECDCVCRNAGG 345

RESULT 9
 ABG76398
 ID ABG76398 standard; protein; 345 AA.
 XX
 AC ABG76398;
 XX
 DT 22-MAY-2003 (first entry)
 XX
 DE Mouse growth factor homologue, zvegfg3.
 XX
 KW Mouse; growth factor homologue; zvegfg3; fibroblast; smooth muscle cell;
 KW cell-surface platelet-derived growth factor alpha receptor; PDGF;
 KW full-thickness skin wound; female reproductive tract; duodenal ulcer;
 KW prolonged bleeding; periodontal disease; tissue adhesive; liver damage;
 KW revascularisation; healing tissue; liver disease; CPC; CHN; cirrhosis;
 KW chronic active hepatitis; hepatic chronic passive congestion; stroke;
 KW central haemorrhagic necrosis; hepatic vein thrombosis; ischaemia;
 KW portal vein thrombosis; cardiac sclerosis; new vessel formation;
 KW endothelial precursor stem cell; neovascularisation; wound healing;
 KW organ transplant; tissue grafting; peripheral neuropathy; spinal cord;
 KW sensory neurite outgrowth; brain damage; head injury; paralysis;
 KW spinal injury; neurodegenerative disease; diabetic retinopathy;
 KW psoriasis; arthritis; scleroderma; keloid; liver fibrosis; psoriasis;
 KW lung fibrosis; kidney fibrosis; glomerulosclerosis; cancer;
 KW proliferative vascular disorder; rheumatoid arthritis; vasculogenesis;
 KW inflammatory disorder; rheumatoid arthritis; vasculogenesis;
 KW angiogenesis; nervous system disorder; cytostatic; hepatotropic;
 KW vulnerary; tranquilliser; cerebroprotective; neuroprotective; nootropic;
 KW ophthalmological; dermatological; coagulant; cardiant.
 XX
 OS Mus musculus.
 XX
 PN US2002177193-A1.
 XX
 PD 28-NOV-2002.
 XX
 PF 02-MAY-2002; 2002US-00139583.
 XX
 PR 07-DEC-1998; 98US-0111173P.
 PR 06-JUL-1999; 98US-0142576P.
 PR 21-OCT-1999; 99US-0161653P.
 PR 12-NOV-1999; 99US-0165255P.
 PR 07-DEC-1999; 99US-00457066.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Gao Z, Hart CE, Piddington CS, Sheppard PO, Shoemaker KE;
 PI Gilbertson DG, West JW;
 XX
 DR WPI; 2003-328485/31.
 DR N-PSDB; ABX93182.
 XX
 PT New isolated zvegfg3 polypeptide, useful for treating cancer, Alzheimer's
 PT disease, Parkinson's disease, chronic active hepatitis, hepatic vein
 PT thrombosis, comprises growth factor domain and CUB domain.
 XX
 PS Claim 1; Fig 6; 73pp; English.
 XX
 CC The present invention relates to the isolation of a growth factor
 CC homologue referred to as zvegfg3, and the polynucleotide sequence encoding
 CC it. The zvegfg3 polypeptide is useful for stimulating the growth of
 CC fibroblasts or smooth muscle cells, or for activating a cell-surface
 CC platelet-derived growth factor (PDGF) alpha receptor. The zvegfg3
 CC polypeptide is useful as a PDGF alpha receptor agonist and thus is useful
 CC for treating full-thickness skin wounds, female reproductive tract and
 CC prolonged bleeding, periodontal disease, damaged liver tissue, and
 CC duodenal ulcers. The polypeptide is also useful as an additive in tissue
 CC adhesives for promoting revascularisation of healing tissue. The zvegfg3
 CC polypeptide is also useful for treating liver damage including damage due
 CC to liver disease, chronic active hepatitis, hepatic chronic passive
 CC congestion (CPC), central haemorrhagic necrosis (CHN), hepatic vein

CC thrombosis, portal vein thrombosis, cardiac sclerosis, and many types of
 CC cirrhosis. The polypeptide is useful for enhancing expansion and
 CC mobilisation of endothelial precursor stem cells, creating and
 CC stabilising new vessel formation in areas requiring neovascularisation,
 CC including areas of ischaemia, organ transplants, wound healing, and
 CC tissue grafting. It may be used for treating peripheral neuropathies by
 CC increasing spinal cord and sensory neurite outgrowth, and as part of
 CC therapeutic treatment for the regeneration of neurite outgrowths
 CC following strokes, brain damage caused by head injuries, and paralysis
 CC caused by spinal injuries. Application may also be made in treating
 CC neurodegenerative diseases (e.g. multiple sclerosis, Alzheimer's disease,
 CC Parkinson's disease), diabetic retinopathy, psoriasis, arthritis,
 CC scleroderma, and reducing fibrosis, keloids, liver fibrosis, lung
 CC fibrosis, kidney fibrosis, and glomerulosclerosis. An antibody that binds
 CC zvegfg3 is useful for blocking the mitogenic, chemotactic, or angiogenic
 CC effects of zvegfg3, and for treating proliferative vascular disorders,
 CC ocular neovascularisation, inflammatory disorders, rheumatoid arthritis,
 CC psoriasis, cancer, impaired or excessive vasculogenesis or angiogenesis,
 CC and diseases of the nervous system. The present sequence represents mouse
 CC zvegfg3

SQ Sequence 345 AA;

Query Match 100.0%; Score 1848; DB 6; Length 345;
 Best Local Similarity 100.0%; Pred. No. 3e-181;
 Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLLTALAGORTGTRAESNLSSKQLSSDKQGVQDPRHRVVTISGNGSIHS 60
 DB 1 MLLGLLLLTALAGORTGTRAESNLSSKQLSSDKQGVQDPRHRVVTISGNGSIHS 60
 QY 61 PKFPHYPRNNMLVWRLVAVDENVRIQLTFDERFGLDEPDDICKYDFVEVEEPSDGSVL 120
 DB 61 PKFPHYPRNNMLVWRLVAVDENVRIQLTFDERFGLDEPDDICKYDFVEVEEPSDGSVL 120
 QY 121 GRWCGSGTVPGKQTSKGNHIRFVSDYFPSPGFCIHYSIIMPQVTTTSPSLPSS 180
 DB 121 GRWCGSGTVPGKQTSKGNHIRFVSDYFPSPGFCIHYSIIMPQVTTTSPSLPSS 180
 QY 181 LSLDLLNNAVTAFSTLEELIRYLPDRQVLDLSLYKETWOLLGKAFLYGKSKVVNLLNL 240
 DB 181 LSLDLLNNAVTAFSTLEELIRYLPDRQVLDLSLYKETWOLLGKAFLYGKSKVVNLLNL 240
 QY 241 LKSEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNCCQVPRK 300
 DB 241 LKSEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNCCQVPRK 300
 QY 301 VTKKYHEVLQRLPKTGKGLHKSITDVALEHHEBCDCVCRGNAGG 345
 DB 301 VTKKYHEVLQRLPKTGKGLHKSITDVALEHHEBCDCVCRGNAGG 345

RESULT 10

ADG47752
 ID ADG47752 standard; protein; 345 AA.

XX
 AC ADG47752;

DT 11-MAR-2004 (first entry)

DE Mouse zvegfg3 protein.

XX Vulnerary; dermatological; wound healing; proliferation; zvegfg3.; mouse.

OS Mus musculus.

XX US6528050-B1.

XX 04-MAR-2003.

XX 06-NOV-2000; 2000US-00706968.

XX 07-DEC-1998; 98US-0111173P.

PR 06-JUL-1999; 99US-0142576P.
 PR 21-OCT-1999; 99US-0161653P.
 PR 12-NOV-1999; 99US-0165253P.
 PR 07-DEC-1999; 99US-00457066.
 PR 31-MAR-2000; 2000US-00541752.
 XX (ZYMO) ZYMOGENETICS INC.
 PA
 PI Gao Z, Hart CE, Piddington CS, Sheppard PO, Shoemaker KE;
 PI Gilbertson DG, West JW;
 XX
 DR WPI; 2003-370630/35.
 DR N-PSDB; ADG47751.
 XX
 XX Promoting wound healing or proliferation of fibroblasts or smooth muscle
 PT cells in a mammal, by administering a polypeptide comprising growth
 PT factor domain of human growth factor homolog polypeptide, zvegfg3.
 XX
 PS Disclosure; SEQ ID NO 43; 69pp; English.
 XX
 CC The present invention relates to a method of promoting wound healing,
 CC especially a dermal wound and for promoting proliferation of fibroblasts
 CC or smooth muscle cells in a mammal, by administering a polypeptide
 CC comprising growth factor domain of human growth factor homolog
 CC polypeptide, zvegfg3. The present sequence is mouse zvegfg3 protein.
 XX
 SQ Sequence 345 AA;
 Query Match 100.0%; Score 1848; DB 7; Length 345;
 Best Local Similarity 100.0%; Pred. No. 3e-181;
 Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLLGLLLLTSAAGQRTGTRAESNLSSKQLQSSDKQNGVQDPHRRVVTISNGSIHS 60
 Db 1 MLLGLLLLTSAAGQRTGTRAESNLSSKQLQSSDKQNGVQDPHRRVVTISNGSIHS 60
 QY 61 PKFPHYPRNMVWRLVAVDENVRITLTFDERFGLDEPDDEICKYDFVEVEPSDGSVL 120
 Db 61 PKFPHYPRNMVWRLVAVDENVRITLTFDERFGLDEPDDEICKYDFVEVEPSDGSVL 120
 QY 121 GRWCSGTVPGKQTSKGNHIRFVSDYFPPSPGFCIHYSIIMPQVTTTSPVLPSS 180
 Db 121 GRWCSGTVPGKQTSKGNHIRFVSDYFPPSPGFCIHYSIIMPQVTTTSPVLPSS 180
 QY 181 LSLLDNLNNAVTAFSTLEELIRYLEPDRQVLDLSLYKPTWQLLKAFLYGKSKVNNL 240
 Db 181 LSLLDNLNNAVTAFSTLEELIRYLEPDRQVLDLSLYKPTWQLLKAFLYGKSKVNNL 240
 QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
 Db 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
 QY 301 VTKKYHEVLQLRPKTGKGLHLSLTDVALEHHEEDCDVCVRNAGG 345
 Db 301 VTKKYHEVLQLRPKTGKGLHLSLTDVALEHHEEDCDVCVRNAGG 345
 RESULT 11
 ADJ32788
 ID ADJ32788 standard; protein; 345 AA.
 XX
 AC ADJ32788;
 XX
 DT 15-APR-2004 (first entry)
 XX
 DE Mouse zvegfg3 protein.
 XX
 KW Growth factor homologue; zvegfg4; skin wound; venous stasis; ulcer;
 KW fracture repair; skin grafting; neovascularisation;
 KW female reproductive tract disorder; bleeding; gastrointestinal tract;
 KW liver damage; hepatic chronic passive congestion; CPC;
 KW central haemorrhagic necrosis; CHN; neurite growth; neuropathy;
 KW neurodegenerative disease; multiple sclerosis; Alzheimer's disease;

KW Parkinson's disease; cell proliferation; cancer; gene therapy; mouse.
 XX Mus sp.
 OS
 XX US2004002140-A1.
 PN
 XX 01-JAN-2004.
 PD
 XX 06-JUN-2001; 2001US-00876813.
 PF
 XX 03-MAY-1999; 99US-0132250P.
 PR 10-NOV-1999; 99US-0164463P.
 PR 04-FEB-2000; 2000US-0180169P.
 PR 03-MAY-2000; 2000US-00564595.
 XX
 XX (GILB/) GILBERT T.
 PA (HART/) HART C E.
 PA (SHEP/) SHEPPARD P O.
 PA (GILB/) GILBERTSON D G.
 XX
 PI Gilbert T, Hart CE, Sheppard PO, Gilbertson DG;
 PI WPI; 2004-070738/07.
 DR N-PSDB; ADJ32787.
 XX
 PT New zvegfg4 polypeptides and nucleic acids, useful for diagnosing or
 PT treating cell loss or abnormal cell proliferation, e.g. cancer, treating
 PT full-thickness skin wounds or treating female reproductive tract
 PT disorders.
 XX
 PS Disclosure; SEQ ID NO 35; 73pp; English.
 XX
 CC The invention relates to growth factor homologue zvegfg4, its
 CC corresponding nucleic acid and methods of using them. The sequences of
 CC the invention are used in the study and regulation of cell and tissue
 CC development, as components of cell culture media and as diagnostic
 CC agents. The zvegfg4 polypeptide can be used in treating full-thickness
 CC skin wounds, including venous stasis, ulcers and other chronic, non-
 CC healing wounds, in fracture repair, skin grafting, in constructive
 CC surgery to promote neovascularisation and increase skin flap survival, to
 CC establish vascular networks in transplanted cells and tissues, or in
 CC treating female reproductive tract disorders, including acute or chronic
 CC placental insufficiency and prolonged bleeding. It can also be used to
 CC promote endothelialisation of vascular grafts and stents, in treating
 CC acute or chronic lesions of the gastrointestinal tract or treating or
 CC repairing liver damage. Zvegfg4 can also be used for treating hepatic
 CC chronic passive congestion (CPC) and central haemorrhagic necrosis (CHN).
 CC Zvegfg4 proteins, agonists and antagonists can also be used to modulate
 CC neurite growth and development and demarcate nervous system structures.
 CC It can also be used for treating peripheral neuropathies or
 CC neurodegenerative diseases including multiple sclerosis, Alzheimer's
 CC disease or Parkinson's disease. The polypeptides, nucleic acids and
 CC antibodies can also be used to diagnose or treat disorders associated
 CC with cell loss or abnormal cell proliferation (including cancer). The
 CC invention is useful in gene therapy. The present sequence is mouse zvegfg3
 CC protein.
 XX
 SQ Sequence 345 AA;
 Query Match 100.0%; Score 1848; DB 8; Length 345;
 Best Local Similarity 100.0%; Pred. No. 3e-181;
 Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLLGLLLLTSAAGQRTGTRAESNLSSKQLQSSDKQNGVQDPHRRVVTISNGSIHS 60
 Db 1 MLLGLLLLTSAAGQRTGTRAESNLSSKQLQSSDKQNGVQDPHRRVVTISNGSIHS 60
 QY 61 PKFPHYPRNMVWRLVAVDENVRITLTFDERFGLDEPDDEICKYDFVEVEPSDGSVL 120
 Db 61 PKFPHYPRNMVWRLVAVDENVRITLTFDERFGLDEPDDEICKYDFVEVEPSDGSVL 120
 QY 121 GRWCSGTVPGKQTSKGNHIRFVSDYFPPSPGFCIHYSIIMPQVTTTSPVLPSS 180
 Db 121 GRWCSGTVPGKQTSKGNHIRFVSDYFPPSPGFCIHYSIIMPQVTTTSPVLPSS 180

Db 121 GRWCSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
QY 181 LSLDLLNNAVTAFTLEELIRYLEPDRMQVDLSLYKPTWQLLGKAFLYGKSKVNLNL 240
Db 181 LSLDLLNNAVTAFTLEELIRYLEPDRMQVDLSLYKPTWQLLGKAFLYGKSKVNLNL 240
QY 241 LKEEVKLYSCTPRNFSVSIRELKRDTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
Db 241 LKEEVKLYSCTPRNFSVSIRELKRDTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
QY 301 VTKKYHEVLQRLPKTGVKGLHKS LTDVALEHHEECDCVCRGNAGG 345
Db 301 VTKKYHEVLQRLPKTGVKGLHKS LTDVALEHHEECDCVCRGNAGG 345

RESULT 12
ADL18359
ID ADL18359 standard; protein; 345 AA.
AC ADL18359;
XX
DT 20-MAY-2004 (first entry)
DE Mouse zveg3 protein.
XX Bone; ligament; cartilage; growth; mouse; zveg3; proliferation;
KW differentiation; osteoblast; osteoclast; chondrocyte;
KW bone marrow stem cell.
XX Mus musculus.
XX
FH Key Location/Qualifiers
FT Region 235..345
FT /note= "Specifically claimed in Claim 1"
XX
PN US2004043031-A1.
XX
PD 04-MAR-2004.
XX
PF 19-SEP-2003; 2003US-00664432.
XX
PR 07-DEC-1999; 98US-00457086.
PR 31-MAR-2000; 2000US-0193723P.
PR 29-MAR-2001; 2001US-00823033.
XX
PA (ZYMO) ZYMOGENETICS INC.
PI Hart CE, Gilbertson DG;
XX
XX WPI; 2004-303322/28.
DR N-PSDB; ADL18358.

PT Promoting growth of bone, ligament or cartilage in mammal involves
PT administering to mammal composition comprising zveg3 dimeric protein and
PT delivery vehicle.
XX
XX Claim 1; SEQ ID NO 4; 31pp; English.
XX
CC The present invention relates to methods for promoting bone, ligament or
CC cartilage growth in a mammal. The methods involve administering to the
CC mammal a composition comprising a dimeric protein of human or mouse
CC zveg3 sequence and a delivery vehicle. Also disclosed are methods for
CC promoting proliferation or differentiation of osteoblasts, osteoclasts,
CC chondrocytes, or bone marrow stem cells. The delivery vehicle is powdered
CC bone, tricalcium phosphate, hydroxyapatite, polymethacrylate,
CC biodegradable polyester, aqueous polymeric gel or fibrin sealant. The
CC methods of the invention are useful for promoting growth of bone,
CC ligament or cartilage in a mammal. The present sequence represents mouse
CC zveg3 protein.
XX
SQ Sequence 345 AA;

Query Match 100.0%; Score 1848; DB 8; Length 345;

Best Local Similarity 100.0%; Pred. No. 3e-181;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGLLLTTSALAGQRTGTRAENLSSKQLQSSDKQNGVQDPRHRRVVTISNGSIHS 60
Db 1 MLLGLLLTTSALAGQRTGTRAENLSSKQLQSSDKQNGVQDPRHRRVVTISNGSIHS 60
QY 61 PKPHTYPRNMVLMVRLVAVDENVRIOITFDERFGLDEPDDICKYDFVEVEEPSDGSVL 120
Db 61 PKPHTYPRNMVLMVRLVAVDENVRIOITFDERFGLDEPDDICKYDFVEVEEPSDGSVL 120
QY 121 GRWCSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
Db 121 GRWCSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
QY 181 LSLDLLNNAVTAFTLEELIRYLEPDRMQVDLSLYKPTWQLLGKAFLYGKSKVNLNL 240
Db 181 LSLDLLNNAVTAFTLEELIRYLEPDRMQVDLSLYKPTWQLLGKAFLYGKSKVNLNL 240
QY 241 LKEEVKLYSCTPRNFSVSIRELKRDTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
Db 241 LKEEVKLYSCTPRNFSVSIRELKRDTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
QY 301 VTKKYHEVLQRLPKTGVKGLHKS LTDVALEHHEECDCVCRGNAGG 345
Db 301 VTKKYHEVLQRLPKTGVKGLHKS LTDVALEHHEECDCVCRGNAGG 345
RESULT 13
AA41766
ID AA41766 standard; protein; 345 AA.
AC AA41766;
XX
DT 07-DEC-1999 (first entry)
DE Human PRO200 protein sequence.
XX
XX Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
KW secreted protein; transmembrane protein.
XX
OS Homo sapiens.
XX WO9946281-A2.
XX
PD 16-SEP-1999.
XX
PF 08-MAR-1999; 98US-0077450P.
XX 10-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
PR 11-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-0077791P.
PR 13-MAR-1998; 98US-0078004P.
PR 17-MAR-1998; 98US-00040220.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078910P.
PR 20-MAR-1998; 98US-0078936P.
PR 20-MAR-1998; 98US-0078939P.
PR 25-MAR-1998; 98US-0079294P.
PR 26-MAR-1998; 98US-0079656P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079684P.
PR 27-MAR-1998; 98US-0079689P.
PR 27-MAR-1998; 98US-0079728P.
PR 27-MAR-1998; 98US-0079786P.
PR 30-MAR-1998; 98US-0079920P.
PR 30-MAR-1998; 98US-0079923P.
PR 31-MAR-1998; 98US-0080105P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080165P.


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PR 31-AUG-1998; 98US-0098548P.
XX (ELIL ) LILLY & CO ELI.
XX PI
XX Dou S, Na S, Song HY;
XX
XX WPI; 1999-458680/38.
XX DR N-PSDB; AAX86352.
XX
XX A vascular endothelial growth factor related protein and related
PT polynucleotide, useful for identifying antagonists and binding compounds.
PT
XX Claim 1; Page 56-58; 62pp; English.
XX
XX The present sequence represents a vascular endothelial growth factor
CC related (VEGF-R) protein. VEGF-R can be used in assays to identify
CC compounds that bind to it or that antagonize its activity. VEGF-R
CC antagonists (e.g. anti-VEGF-R antibodies) are useful for inhibiting
CC tissue growth. This is useful for inhibiting tumour growth and for
CC treating cancer. VEGF-R itself can be used to stimulate tissue growth,
CC angiogenesis and to treat coronary artery blockage. The VEGF-R coding
CC sequence can be used for the recombinant production of the VEGF-R protein
XX
SQ Sequence 345 AA;
Query Match 90.2%; Score 1667; DB 2; Length 345;
Best Local Similarity 87.0%; Pred. No. 1.4e-162;
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;
QY 1 MLLGLLLTTSALAGQRTGTRAESNLSSKQLSSDKQNGVQDPRHVRVITSGNGSIHS 60
DB 1 MSLFGLLLTTSALAGQRTGTRAESNLSSKQLSSDKQNGVQDPRHVRVITSGNGSIHS 60
QY 61 PRPHTYPRNMVLRVAVDENVRIQLTFDERFGLDEPDDEICKYDFVEEPEPSDGSVL 120
DB 61 PRPHTYPRNTVLRVAVDENVRIQLTFDERFGLDEPDDEICKYDFVEEPEPSDGSVL 120
QY 121 GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTTTSPSLPPSS 180
DB 121 GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTTTSPSLPPSS 180
QY 181 LSLDLLNNAVTAFTSTLEELIRVLEPDRQVLDLSLYKPTWQLLKAFYKSKSVNLNL 240
DB 181 LPLDLLNNAITAFSTLEDLIRYLEPERWQLDLELYRPTWQLLKAFYKSKSVNLNL 240
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPK 300
DB 241 LTEEVRVLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPK 300
QY 301 VTKKYHEVLQRPKTVGKGLHKLSTDLVALEHHEECDCVCRGNAGG 345
DB 301 VTKKYHEVLQRPKTVGKGLHKLSTDLVALEHHEECDCVCRGNAGG 345
RESULT 15
AAY33679
XX ID AAY33679 standard; protein; 345 AA.
XX AC AAY33679;
XX
XX DT 11-JAN-2000 (first entry)
XX
XX DE Human VEGF-E protein.
XX
XX KW VEGF-E; human; vascular endothelial cell growth factor; wound repair;
KW treatment; cardiovascular disorder; endothelial disorder; therapy;
KW tissue generation; regeneration; cardiac hypertrophy; cancer; detection;
KW angiogenic disorder; age-related macular degeneration; vascular disease;
KW neovascularization; tumor; gene mapping.
XX
XX OS Homo sapiens.
XX
XX PN W09947677-A2.

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XX 23-SEP-1999.
XX
XX 10-MAR-1999; 99WO-US005190.
XX
XX 17-MAR-1998; 98US-00040220.
XX 02-NOV-1998; 98US-00184216.
XX (GETH ) GENENTECH INC.
XX
XX Ferrara N, Kuo SS;
XX
XX WPI; 1999-580306/49.
XX DR N-PSDB; AAZ23691.
XX
XX New growth factor polypeptide useful for treating cardiovascular or
XX endothelial disorders, e.g. cardiac hypertrophy.
XX
XX Claim 1; Fig 2; 122pp; English.
XX
XX This invention describes the isolation of a novel human vascular
XX endothelial cell growth factor-E (VEGF-E) polypeptide which has
XX tranquilizer, vulnery and cardiant activity. VEGF-E can be administered
XX therapeutically, especially by expressing encoding polynucleotides, to
XX treat cardiovascular or endothelial disorders in mammals, especially
XX humans. It is useful in wound repair and tissue generation and
XX regeneration, and may especially be used to treat cardiac hypertrophy It
XX can be combined with a carrier in pharmaceutical compositions, which can
XX be administered to treat disorders as above. VEGF-E can be used to screen
XX for antagonists and agonists, and the antagonists administered to treat
XX angiogenic disorders in mammals (especially humans) e.g. cancer or age-
XX related macular degeneration. It can be used to generate antibodies,
XX useful therapeutically as antagonists, as above. The antibodies are also
XX useful to detect VEGF-E polypeptide, especially to diagnose
XX cardiovascular, endothelial or angiogenic disorders in mammals (e.g.
XX vascular disease, or neovascularization associated with tumor formation),
XX by contacting the antibody with a tissue sample and detecting formation
XX of an antibody-VEGF-E polypeptide complex. Polynucleotides encoding VEGF-
XX E can be used to diagnose cardiovascular and endothelial disorders in
XX mammals, by detecting abnormally high or low VEGF-E gene expression in
XX tissue samples. They can also be used to diagnose a disease or
XX susceptibility to a disease related to a mutated form of VEGF-E (e.g. a
XX cardiovascular, endothelial or angiogenic disorder such as a tumor), by
XX detecting a mutation in the VEGF-E-encoding sequence isolated from a
XX sample. They may also be used to produce probes useful to detect related
XX sequences or for gene mapping. This sequence represents the human VEGF-E
XX protein described in the method of the invention
XX
SQ Sequence 345 AA;
Query Match 90.2%; Score 1667; DB 2; Length 345;
Best Local Similarity 87.0%; Pred. No. 1.4e-162;
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;
QY 1 MLLGLLLTTSALAGQRTGTRAESNLSSKQLSSDKQNGVQDPRHVRVITSGNGSIHS 60
DB 1 MSLFGLLLTTSALAGQRTGTRAESNLSSKQLSSDKQNGVQDPRHVRVITSGNGSIHS 60
QY 61 PRPHTYPRNMVLRVAVDENVRIQLTFDERFGLDEPDDEICKYDFVEEPEPSDGSVL 120
DB 61 PRPHTYPRNTVLRVAVDENVRIQLTFDERFGLDEPDDEICKYDFVEEPEPSDGSVL 120
QY 121 GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTTTSPSLPPSS 180
DB 121 GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTTTSPSLPPSS 180
QY 181 LSLDLLNNAVTAFTSTLEELIRVLEPDRQVLDLSLYKPTWQLLKAFYKSKSVNLNL 240
DB 181 LPLDLLNNAITAFSTLEDLIRYLEPERWQLDLELYRPTWQLLKAFYKSKSVNLNL 240
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPK 300
DB 241 LTEEVRVLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPK 300

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Qy 301 VTKKYHEVLQLRPKTGVKGLHKSLTDVALEHHHECDCVCRGNAGG 345
Db 301 VTKKYHEVLQLRPKTGVKGLHKSLTDVALEHHHECDCVCRGSTGG 345

Search completed: September 3, 2005, 19:25:51
Job time : 122.5 sec8

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 3, 2005, 19:17:40 ; Search time 25.5 Seconds
(without alignments)
1301.756 Million cell updates/sec

Title: US-09-818-943-2
Perfect score: 1848
Sequence: 1 MLLGLLLLTALAGQRTGT.....DVALEHHEECDCVCKGNAGG 345
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	754	40.8	370	2	JC7592
2	753	40.7	370	2	spinal cord-derive
3	746.5	40.4	370	2	platelet-derived g
4	191	10.3	707	2	JC7998
5	190	10.3	823	1	procollagen C-endo
6	183.5	9.9	927	1	procollagen C-endo
7	183.5	9.9	927	1	A5 antigen precurs
8	181	9.8	986	1	procollagen C-endo
9	181	9.8	991	2	procollagen C-endo
10	174.5	9.4	3623	2	T09456
11	160	8.7	3623	2	intrinsic factor-B
12	158	8.5	449	2	procollagen I C-pr
13	153	8.3	1057	1	dorsal-ventral pat
14	147.5	8.0	1524	2	polyprotein - Afri
15	145.5	7.9	686	1	Ra-reactive factor
16	144	7.8	699	1	Ra-reactive factor
17	143.5	7.8	597	2	S71352
18	141.5	7.7	1070	2	T31069
19	140.5	7.6	3871	2	T22812
20	139	7.5	1594	2	T30549
21	137.5	7.4	705	1	CHIURB
22	135.5	7.3	1464	2	S58984
23	133.5	7.2	402	2	JH0403
24	128	6.9	277	2	A41735
25	127	6.9	419	2	S69207
26	126.5	6.8	579	2	JC7629
27	125.5	6.8	245	1	TVC2SS
28	125.5	6.8	767	2	J30018
29	125	6.8	533	2	JC7985

30 123 6.7 275 2 JC6506 tumor necrosis fac
31 122.5 6.6 2403 2 A59386 sanko - human
32 119.5 6.5 2083 2 T42721 CRP-ductin-alpha p
33 117.5 6.4 276 2 A47290 TSG-6 homolog PS4
34 117.5 6.4 1290 2 A57190 ebnerin precursor
35 114.5 6.2 200 2 I51551 platelet-derived g
36 114.5 6.2 215 2 S08220 platelet-derived g
37 114.5 6.2 226 2 I51550 platelet-derived g
38 113 6.1 695 1 S05008 complement subcomp
39 112.5 6.1 241 1 PFHUG2 platelet-derived g
40 111.5 6.0 226 1 TVMVSS PDGF-related trans
41 109 5.9 694 2 JC6554 complement subcomp
42 108.5 5.9 148 2 D49530 16k vascular endot
43 107 5.8 321 2 T33161 hypothetetical prote
44 104 5.6 319 2 I51569 UVS.2 protein - Af
45 103.5 5.6 225 2 S25097 platelet-derived g

ALIGNMENTS

RESULT 1
JC7592
spinal cord-derived growth factor-B precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C:Accession: JC7592
R:Hamada, T.; Ui-Tei, K.; Imaki, J.; Miyata, Y.
Biochem. Biophys. Res. Commun. 280, 733-737, 2001
A:Title: Molecular cloning of SCDGF-B, a novel growth factor homologous to SCDGF/PDGF-C/
A:Reference number: JC7591; MUID:21092670; PMID:11162582
A:Contents: Fetal brain
A:Accession: JC7592
A:Molecule type: mRNA
A:Residues: 1-370 <HAM>
A:Cross-references: UNIPROT:Q9EQT1; DBJ:AB052170
C:Genetics:
A:Gene: scdGF-B
F:1-17/Domain: secretory signal sequence #status predicted <SIG>
F:18-370/Product: spinal cord-derived growth factor-B #status predicted <MAT>
F:52-170/Region: CUB domain #status predicted
F:272-370/Region: homologous to platelet-derived growth factor/vascular endothelial grow
F:294-308/Region: conserved motif #status predicted

Query Match	40.8%	Score 754;	DB 2;	Length 370;
Best Local Similarity	46.2%	Pred. No. 8.2e-55;		
Matches 151;	Conservative 62;	Mismatches 86;	Indels 28;	Gaps 10;
Qy	37	EQNGVQD-PRHVVVTISNGSIHSKPFPHYPRNMVLMVRLVAVDENVRQLTFDERFG	95	
Db	42	ESNHLTDLRRDENIRVTGTGHVQSPRPFPNSYPRNLLLTWRLHS-QEKTRIQLAFDHQFG	100	
Qy	96	LEDDEDDICKYDFVEVEPSPDGS--VLGRWCGSGTVPGKQTSKGNHRIHFVSDEYFPSE	153	
Db	101	LEEAENICRYDFVEVEDVSESSTVVRGWCGHKEIPRITSRTNQIKITFQSDDYFVAK	160	
Qy	154	PGFCHYSII---MPQ-----VTET-----TPSVLPSPSSLSLDLNNVATFST	195	
Db	161	PGFKIYTSFVEDFQFEAAEINWESVTSFSGVSYHSPSVM-DSTLTADADKAIAEDT	219	
Qy	196	LEEIRYLEPDRQWDLDSLYKPTWQLLGKAFKYGKSKSVNLLKKEVKLYSCTPRNF	255	
Db	220	VEDLLKYFNPASWQDDLLENLYMDTPRYGRSY-HERKSK-VDLRLNDVVKRYSCTPRNH	277	
Qy	256	SVSTRRELKRTDTTFWPGCLLVKCGGCACCLHNCQCQVPRKYTKYHVLQLRP--	313	
Db	278	SWNREELKLTNAVFPFRCLLVQRCGNCGGTLNWKSCCTSSGKTVKXKHYEVLKPEFGH	337	
Qy	314	-KTGVKGLHSLTDVALEHHEECDCVC	339	
Db	338	FRRGKAKMALVDIQDHERCDCIC	364	

RESULT 2
 JC7591
 spinal cord-derived growth factor-B precursor - human
 C:Species: Homo sapiens (man)
 C>Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
 C:Accession: JC7591
 R:Hamada, T.; Uti-Tel, K.; Imaki, J.; Miyata, Y.
 Biochem. Biophys. Res. Commun. 280: 733-737, 2001
 A:Title: Molecular cloning of SCDF-B, a novel growth factor homologous to SCDF/PDGF-C
 A:Reference number: JC7591; PMID:21092670; PMID:11162582
 A:Accession: JC7591
 A:Molecule type: DNA
 A:Residues: 1-370 <HAM>
 A:Cross-references: UNIPROT:Q9BWV5; UNIPROT:Q9GZP0; DDBJ:AB033832
 C:Genetics:
 F:1-17/Domain: secretory signal sequence #status predicted <SIG>
 F:18-370/Product: spinal cord-derived growth factor-B #status predicted <MAT>
 F:52-170/Region: CUB domain #status predicted
 F:272-370/Region: homologous to platelet-derived growth factor/vascular endothelial growth factor
 F:294-308/Region: conserved motif #status predicted

Query Match 40.7%; Score 753; DB 2; Length 370;
 Best Local Similarity 45.3%; Pred. No. 9.9e-55;
 Matches 148; Conservative 59; Mismatches 92; Indels 28; Gaps 9;

QY 37 EQNGVQD-PRHVVTVISNGSIHSPKPPHTYPRNMVLVRLVAVDENVRIQLTFDERPG 95
 DB 42 ESNHLTDLRYRDETQVKGNGVQSPFPNSYPRNLLLTWRLHS-QENTRIQLVDFDNOFG 100

QY 96 LEDPDDICKYDFVEVEPSDGLV--GRWCGSGVPGKQTSKGNHRIKRVFVSDYFVPS 153
 DB 101 LBEAENDICRYDFVEVEDISESTIIRGNWCGHEVPPRIKRTQIKITFKSDDYFVAK 160

QY 154 PGFCIHYSII---MPQVTETT-----SPSVLPSSLSLDDLNNVAVTAFST 195
 DB 161 PGFKIVYSLLDFQPAASSETNWESVTSISGVSNPSVTDTP-TLIADALDKIAEFD 219

QY 196 LBEILRYLEPDRQVLDLSLYKPTWQLLGKAFLYKKSKVNLNLLKEEVLYSCTPRNF 255
 DB 220 VDLRLKYFPESQWEDLENMVLDTPTRYGRSY-HSRKSK-VDLDRDLNDDAKRYSCPT 277

QY 256 SVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRKVTYKHYEVLQLRP-- 313
 DB 278 SVNIREELKLANVFPFRCLLVQRCGNGCGCTVNRSTCNSGKTVKHYEVLQFEPOH 337

QY 314 -KTGVKGLHKSJTDVALEHHEECDCVC 339
 DB 338 IKRRGRKTMALVDIQLDHHERCDCIC 364

RESULT 3
 JC7998
 platelet-derived growth factor-D - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 10-Nov-2003 #sequence_revision 10-Nov-2003 #text_change 24-Nov-2003
 C:Accession: JC7998
 R:Zhao, Y.; Hoyie, G.W.; Zhang, J.; Morris, G.; Lasky, J.A.
 Biochem. Biophys. Res. Commun. 308: 126-132, 2003
 A:Title: A novel murine PDGF-D splicing variant results in significant differences in pe
 A:Reference number: JC7998; PMID:12890490
 A:Accession: JC7998
 A:Molecule type: mRNA
 A:Residues: 1-370 <ZHU>
 C:Comment: This protein is a potent mesenchymal cell mitogen and chemoattractant involve
 C:Genetics:
 A:Gene: pdgf-D
 A:Introns: 42/2; 110/1; 170/2; 191/2; 258/2; 330/1; 334/2
 C:Keywords: fibrosis; PDGF-D

Query Match 40.4%; Score 746.5; DB 2; Length 370;
 Best Local Similarity 43.5%; Pred. No. 3.4e-54;
 Matches 151; Conservative 63; Mismatches 102; Indels 31; Gaps 9;

QY 16 QRTGTRAESNLSSKQLQSSDKQNGVQDPRHVVTVISNGSIHSPKPPHTYPRNMVLVW 75
 DB 26 QRASIKALRNAN-----LRRDESNLHLDLYQREENIQVTNSNGHVQSPFPNSYPRNLLLTW 81

QY 76 RLVAVDENVRIQLTFDERFGLDEDDICKYDFVEVEPSDGLS--VLGRWCGSGTVPGKQ 133
 DB 82 WLRS-QEKTRIQLSDFDQFGLBEAENDICRYDFVEVEVESSSTVVRGWCGHKEIPRI 140

QY 134 TSKGNHRIKRVFVDEYPPSPGFCIHYSII---MPQVTETT-----SPSV 175
 DB 141 TSRTNQIKITPKSDDYFVAKPGFKIYYSFVDFQPEAASSETNWESVTSSFSGVSVHSPSI 200

QY 176 LPPSSLSLDDLNNVAVTAFSTLEELIRYLEPDRQVLDLSLYKPTWQLLGKAFLYKKSKV 235
 DB 201 TDP-TLTADALDKTVAEPDVTEDLLKHFPNSVQDDLENLYLDTPHYGRSY-HDRKSK- 257

QY 236 VNLMLKEEVLYSCTPRNFVSIREELKRYDTTFWPGCLLVKRCGNCACCLHNCNECQ 295
 DB 258 VDLRLNDVVKRYSCPTPRNHSVNLREELKLTNAVFFPRCLLVQRCGNGCGTVMWKSCT 317

QY 296 CVPRKVTYKHYEVLQLRP---KTGVKGLHKSJTDVALEHHEECDCVC 339
 DB 318 CSSGKTVKHYEVLKFEFGHFRGRGAKAKMALVDIQLDHHERCDCIC 364

RESULT 4
 JC2218
 procollagen C-endopeptidase (EC 3.4.24.19) - African clawed frog (clone 22AN)
 N:Alternate names: bone morphogenic protein 1
 C:Species: Xenopus laevis (African clawed frog)
 C>Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 09-Jul-2004
 C:Accession: JC2218
 R:Maeno, M.; Xue, Y.; Wood, T.I.; Ong, R.C.; Kung, H.
 A:Title: Cloning and expression of cDNA encoding Xenopus laevis bone morphogenetic prote
 A:Reference number: JC2218; PMID:94085787; PMID:8262384
 A:Accession: JC2218
 A:Molecule type: mRNA
 A:Residues: 1-707 <MA>
 A:Cross-references: UNIPROT:P98070; GB:L12249; NID:9406540; PIDN:AAA16313.1; PID:9406541
 C:Comment: This protein induces ectopic cartilage formation in vivo.
 C:Superfamily: procollagen C-endopeptidase; astacin homology; C1r/C1s repeat homology; zinc
 C:Keywords: beta-hydroxyasparagine; glycoprotein; hydrolase; metalloproteinase; zinc
 F:93-284/Domain: astacin homology <AST>
 F:285-397/Region: complement 1r/1s-like repeat
 F:285-394/Domain: C1r/C1s repeat homology <C1R1>
 F:398-510/Region: complement 1r/1s-like repeat
 F:398-507/Domain: C1r/C1s repeat homology <C1R2>
 F:514-550/Domain: EGF homology <EGF>
 F:554-666/Region: complement 1r/1s-like repeat
 F:554-663/Domain: C1r/C1s repeat homology <C1R3>
 F:62.105,295,326/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:176,180,186,235/Binding site: zinc (His, His, His, Tyr) #status predicted
 F:177/Active site: Glu #status predicted
 F:528/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match 10.3%; Score 191; DB 2; Length 707;
 Best Local Similarity 45.2%; Pred. No. 9.7e-08;
 Matches 47; Conservative 16; Mismatches 33; Indels 8; Gaps 5;

QY 55 NGSTHSPKPPHTYPRNMVLVRLVAVDENVRIQLTFDERFGLDEDDICKYDFVEVEE- 113
 DB 562 NGSINSPGWPKYPPNKNKCIQWLVAPTQ-YRISLKFDQ---FETEGNDVCKYDFVEVRSG 617

QY 114 -PSDGSVLGRWCGSGTVPGKQTSKGNHRIKRVFVSDYFVPSPGF 156
 DB 618 LTSDSKLHGKFCGS-ELPAVITTSQYNNMRIFBKSDNTV-SKKGF 659

RESULT 5
 A58788
 procollagen C-endopeptidase (EC 3.4.24.19) precursor, splice form HIS - human

N:Alternate names: bone morphogenic protein splice form BMP-1/His
C:Species: Homo sapiens (man)
C:Date: 28-Mar-1998 #sequence_revision 09-Apr-1998 #text_change 18-Jun-1999
C:Accession: A37278; A58788
R:Woźney, J.M.; Rosen, V.; Celeste, A.J.; Mitscock, L.M.; Whitters, M.J.; Kriz, R.W.; Hew
Science 242, 1528-1534, 1988
A:Title: Novel regulators of bone formation: molecular clones and activities.
A:Reference number: A37278; MUID:89072730; PMID:3201241
A:Accession: A37278
A:Molecule type: mRNA
A:Residues: 1-702, 'EXPPALQPRGRPHQLKFRVQKNRTPO' <WO2>
A:Cross-references: GB:M22488; NID:g179499; PIDN:AAA51833.1; PID:g179500
R:Takahara, K.; Lyons, G.E.; Greenspan, D.S.
J. Biol. Chem. 269, 32572-32578, 1994
A:Title: Bone morphogenetic protein-1 and a mammalian tolloid homologue (mTld) are encoded
A:Reference number: A58788; MUID:95096114; PMID:7798260
A:Accession: A58788
A:Molecule type: mRNA
A:Residues: 703-823 <TAK>
A:Cross-references: GB:M22488; NID:g179499; PIDN:AAA51833.1; PID:g179500
C:Genetics:
A:Gene: GDB:BMP1; BMP-1
A:Cross-references: GDB:125203; OMIM:112264
C:Function:
A:Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen type
C:Superfamily: procollagen C-endopeptidase; astacin homology; C1r/C1s repeat homology; E
C:Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; gl
F:1-22/Domain: signal sequence #status predicted <SIG>
F:123-823/Product: procollagen C-endopeptidase splice form HIS #status predicted <MAT>
F:130-321/Domain: astacin homology <AST>
F:322-431/Domain: C1r/C1s repeat homology <C1R1>
F:435-544/Domain: C1r/C1s repeat homology <C1R2>
F:551-587/Domain: EGF homology <EGF>
F:591-700/Domain: C1r/C1s repeat homology <C1R3>
F:738-752/Region: histidine-rich
F:91,142,332,363,599/Binding site: carboxylate (Asn) (covalent) #status predicted
F:163-319,185-205,322-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,644-66
F:213,217,223,272/Binding site: zinc (His, His, His, Tyr) #status predicted
F:214/Active site: Glu #status predicted
F:565/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match 10.3%; Score 190; DB 1; Length 823;
Best Local Similarity 36.0%; Pred. No. 1.4e-07;
Matches 54; Conservative 20; Mismatches 48; Indels 28; Gaps 7;
Qy 55 NGSITSPKFPHTYPRNMVLRVAVDENVRILQTFDERFGLDEPDICKYDFVEVEE- 113
Db 599 NGSITSPGWPKKEYPPNKNCIWQVAPTO-YRISLQFD---FFETEGNDVCKYDFVEVRSG 654
Qy 114 -PSDGSVLGRWCGSGTVPKQTSKGNHRIIRFVSDYPPSPGFCIHV----- 160
Db 655 LTADSKLHGKFCGS-EKPEVITSQYNNRNVFKSDNTV-SKKGPKAHFFSVLEAGDRHS 712
Qy 161 -----SIIMQVTTTSPVLPSSLSLD 184
Db 713 HLSGLELLCPHALVDTPVA--PPSALHGD 740

RESULT 6
BMHUI
procollagen C-endopeptidase (EC 3.4.24.19) precursor, splice form BMP1 - human
N:Alternate names: bone morphogenic protein 1 (BMP1)
C:Species: Homo sapiens (man)
C:Date: 16-Sep-1992 #sequence_revision 03-Aug-1995 #text_change 18-Jun-1999
C:Accession: A37278; E58788
R:Woźney, J.M.; Rosen, V.; Celeste, A.J.; Mitscock, L.M.; Whitters, M.J.; Kriz, R.W.; Hew
Science 242, 1528-1534, 1988
A:Title: Novel regulators of bone formation: molecular clones and activities.
A:Reference number: A37278; MUID:89072730; PMID:3201241
A:Accession: A37278
A:Molecule type: mRNA
A:Residues: 1-730 <WO2>

A:Cross-references: GB:M22488; NID:g179499; PIDN:AAA51833.1; PID:g179500
C:Genetics:
A:Gene: GDB:BMP1
A:Cross-references: GDB:125203; OMIM:112264
A:Map position: 8p21-8p21
C:Function:
A:Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen type
C:Superfamily: procollagen C-endopeptidase; astacin homology; C1r/C1s repeat homology; E
C:Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; gl
F:1-22/Domain: signal sequence #status predicted <SIG>
F:123-823/Product: procollagen C-endopeptidase splice form BMP1 #status predicted <MAT>
F:130-321/Domain: astacin homology <AST>
F:322-431/Domain: C1r/C1s repeat homology <C1R1>
F:435-544/Domain: C1r/C1s repeat homology <C1R2>
F:551-587/Domain: EGF homology <EGF>
F:591-700/Domain: C1r/C1s repeat homology <C1R3>
F:91,142,332,363,599/Binding site: carboxylate (Asn) (covalent) #status predicted
F:163-319,185-205,322-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,644-66
F:213,217,223,272/Binding site: zinc (His, His, His, Tyr) #status predicted
F:214/Active site: Glu #status predicted
F:565/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match 9.9%; Score 183.5; DB 1; Length 730;
Best Local Similarity 38.9%; Pred. No. 4.2e-07;
Matches 49; Conservative 18; Mismatches 44; Indels 15; Gaps 6;
Qy 55 NGSITSPKFPHTYPRNMVLRVAVDENVRILQTFDERFGLDEPDICKYDFVEVEE- 113
Db 599 NGSITSPGWPKKEYPPNKNCIWQVAPTO-YRISLQFD---FFETEGNDVCKYDFVEVRSG 654
Qy 114 -PSDGSVLGRWCGSGTVPKQTSKGNHRIIRFVSDYPPSPGFCIHVSIIMQVTTTTS 172
Db 655 LTADSKLHGKFCGS-EKPEVITSQYNNRNVFKSDNTV-SKKGPKAHF-----FSEK 705
Qy 173 PSVLPP 178
Db 706 PALQPP 711

RESULT 7
JQ0948
A5 antigen precursor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C:Accession: JQ0466; JQ0948
R:Takagi, S.; Hirata, T.; Agata, K.; Mochii, M.; Eguchi, G.; Fujisawa, H.
Neuron 7, 295-307, 1991
A:Title: The A5 antigen, a candidate for the neuronal recognition molecule, has homology
A:Reference number: JQ0466; MUID:91337458; PMID:1908252
A:Accession: JQ0466
A:Molecule type: mRNA
A:Residues: 1-927 <TAK>
A:Cross-references: GB:D10467; GB:D01077; NID:g2222962; PIDN:BAA01260.1; PID:g222963
A:Experimental source: tadpole, brain
A:Note: This protein has motifs homologous to complement components C1r and C1s and to c
C:Comment: This protein is a neuronal cell surface molecule involved in the neuronal rec
C:Superfamily: Xenopus A5 antigen; C1r/C1s repeat homology; discoidin I amino-terminal h
C:Keywords: duplication; glycoprotein; transmembrane protein
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-927/Product: A5 antigen #status predicted <ASA>
F:27-138/Domain: C1r/C1s repeat homology <C1R1>
F:147-262/Domain: discoidin I amino-terminal homology <C1R2>
F:274-424/Domain: discoidin I amino-terminal homology <DN1>
F:430-584/Domain: discoidin I amino-terminal homology <DN2>
F:646-812/Domain: MAM homology <MAM>
F:861-883/Domain: transmembrane #status predicted <TM>
F:150,261,300,523,844/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.9%; Score 183.5; DB 1; Length 927;
Best Local Similarity 30.7%; Pred. No. 5.7e-07;
Matches 55; Conservative 34; Mismatches 65; Indels 25; Gaps 9;
Qy 50 VTISNGSIHSPKFPHTYPRNMVLRVAVDENVRILQTFDERFGLDEPDICKYDFV 109

Db 31 IKITSPSLTSGYSHSPQRCWELQAEHYIRIMNPNFPLEDRE--CKYDYV 87
QY 110 EV--EERSDGSVLGRWCSSGTVPGKQTKGNHIRIRFVDSYFSPGFCIHYSIIM--P 165
Db 88 EVIDGDNAGQLLGYCKG-IAPSPLVSTGSPFIRFVSDYETPG-AGFSIRYEVFKTGP 145
QY 166 QVTE--TWTSPSLP-----PSSLSDLLNNAVTAFTLEELIRVLEPDRMQVDLDS 214
Db 146 ECSRNFTSSNGVIKSPKPEKYPNALECTYIFA-----PRMQEIV--LEFSSFELEADS 198
RESULT 8
B58788
procollagen C-endopeptidase (EC 3.4.24.19) precursor, tolloid-like splice form - human
N:Alternate names: bone morphogenic protein 1, tolloid-like splice form
C:Species: Homo sapiens (man)
C>Date: 28-Mar-1998 #sequence_revision 09-Apr-1998 #text_change 09-Jul-2004
R:Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mitsock, L.M.; Whitters, M.J.; Kriz, R.W.; Hew
Science 242, 1528-1534, 1988
A>Title: Novel regulators of bone formation: molecular clones and activities.
A:Reference number: A37278; MUID:89072730; PMID:3201241
A:Accession: A37278
A:Molecule type: mRNA
A:Residues: 1-702, 'EKPALQPPRGPHQLKFRVQKRNTPQ' <WOZ>
A:Cross-references: UNIPROT:P13497; GB:W22486; NID:gl79499; PIDN:AAA51833.1; PID:gl79500
R:Takahara, K.; Lyons, G.E.; Greenspan, D.S.
J. Biol. Chem. 269, 32572-32578, 1994
A>Title: Bone morphogenetic protein-1 and a mammalian tolloid homologue (mtld) are encod
A:Reference number: A58788; MUID:95096114; PMID:7798260
A:Accession: B58788
A:Molecule type: mRNA
A:Residues: 703-986 <TAK>
A:Cross-references: GB:L35279; NID:g619860; PIDN:AAC41710.1; PID:g619861
C:Genetics:
A:Gene: GDB:BMPL; BMP-1
A:Cross-references: GDB:125203; OMIM:112264
A:Map position: 8p21-8p21
C:Function:
A:Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen type
C:Superfamily: procollagen C-endopeptidase; astacin homology; C1r/C1s repeat homology; E
C:Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; gl
F:1-22/Domain: signal sequence #status predicted <SIG>
F:223-986/Product: procollagen C-endopeptidase tolloid-like splice form #status predicted
F:130-321/Domain: astacin homology <AST>
F:322-431/Domain: C1r/C1s repeat homology <C1R1>
F:435-544/Domain: C1r/C1s repeat homology <C1R2>
F:551-587/Domain: EGF homology <EG1>
F:591-700/Domain: C1r/C1s repeat homology <C1R3>
F:707-742/Domain: EGF homology <EG2>
F:747-856/Domain: C1r/C1s repeat homology <C1R4>
F:860-973/Domain: C1r/C1s repeat homology <C1R5>
F:91-142,332,363,599/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:163-319,185-205,322-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,644-66
F:213,217,223,272/Binding site: zinc (His, His, His, Tyr) #status predicted
F:214/Active site: Glu #status predicted
F:565,720/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
Query Match 9.8%; Score 181; DB 1; Length 986;
Best Local Similarity 42.6%; Pred. No. 9.9e-07;
Matches 46; Conservative 16; Mismatches 38; Indels 8; Gaps 5;
QY 55 NGSIHSPKPPHTYPRNMVLVRLVAVDENVRIQLTFDERFGLEDDEDDICKYDFVEVEE- 113
Db 599 NGSITSPGWPKPEYPPNKNCIWLVAPTQ-YRISLQFD---PFTEGNDVCKYDFVEVRSG 654
QY 114 -PSDGSVLGRWCSSGTVPGKQTKGNHIRIRFVDSYFSPGFCIH 160
Db 655 LTADSKLHGKFCGS-EKPEVITSQNNMRVEFKSDNTV-SKKGFKAHF 700
RESULT 9

149540
procollagen C-endopeptidase (EC 3.4.24.19) precursor, tolloid-like splice form - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I49540
R:Fukagawa, M.; Noboru, S.; Hogan, B.L.M.; Jones, C.M.
Dev. Biol. 163, 175-183, 1994
A>Title: Embryonic expression of mouse bone morphogenetic protein-1 (BMP-1) which is rel
A:Reference number: I49540; MUID:94229342; PMID:8174772
A:Accession: I49540
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-991 <RES>
A:Cross-references: UNIPROT:P98063; GB:L24755; NID:g439606; PIDN:AAA37306.1; PID:g439607
C:Genetics:
A:Gene: Bmp-1
C:Superfamily: procollagen C-endopeptidase; astacin homology; C1r/C1s repeat homology; E
C:Keywords: hydrolase; metalloproteinase; zinc
F:135-326/Domain: astacin homology <AST>
F:556-592/Domain: EGF homology <EG1>
F:596-705/Domain: C1r/C1s repeat homology <C1R>
F:712-747/Domain: EGF homology <EG2>
F:218,222,228,277/Binding site: zinc (His, His, His, Tyr) #status predicted
F:219/Active site: Glu #status predicted
Query Match 9.8%; Score 181; DB 2; Length 991;
Best Local Similarity 42.6%; Pred. No. 1e-06;
Matches 46; Conservative 16; Mismatches 38; Indels 8; Gaps 5;
QY 55 NGSIHSPKPPHTYPRNMVLVRLVAVDENVRIQLTFDERFGLEDDEDDICKYDFVEVEE- 113
Db 604 NGSITSPGWPKPEYPPNKNCIWLVAPTQ-YRISLQFD---PFTEGNDVCKYDFVEVRSG 659
QY 114 -PSDGSVLGRWCSSGTVPGKQTKGNHIRIRFVDSYFSPGFCIH 160
Db 660 LTADSKLHGKFCGS-EKPEVITSQNNMRVEFKSDNTV-SKKGFKAHF 705
RESULT 10
T09456
intrinsic factor-B12 receptor Cubilin precursor - human
C:Species: Homo sapiens (man)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T09456
R:Kozyraki, R.; Kistiansen, M.; Silahataroglu, A.; Hansen, C.; Tommerup, N.
Blood 91, 3593-3600, 1998
A>Title: The human intrinsic factor-vitamin B12 receptor, cubilin: Molecular characteriz
ion.
A:Reference number: Z16677; MUID:98241400; PMID:9572993
A:Accession: T09456
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-3623 <KOZ>
A:Cross-references: UNIPROT:O60494; EMBL:AF034611; NID:g3929528; PIDN:AAC82612.1; PID:g3
C:Genetics:
A:Map position: 10p12
C:Superfamily: intrinsic factor-B12 receptor cubilin; EGF homology
C:Keywords: receptor; vitamin B12 uptake
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-3623/Product: intrinsic factor-B12 receptor #status predicted <MAT>
F:436-467/Domain: EGF homology <EGF>
Query Match 9.4%; Score 174.5; DB 2; Length 3623;
Best Local Similarity 31.9%; Pred. No. 1.8e-05;
Matches 53; Conservative 26; Mismatches 64; Indels 23; Gaps 8;
QY 15 QORTGTAEENLSSK-----LQLSSD--KEQGVQDPRHERVVTISNGNSIH----- 59
Db 2173 GHFCGSHASSTLTFTSDNQMFQFISDHNEQGQFKIYEAKSLACGGNVYIHDAASGYV 2232
QY 60 -SPKPPHTYPRNMVLVRLVAVDENVRIQLTFDERFGLEDDEDDICKYDFVEVEE--PSD 116
Db 2233 TSPNHPHNPYPHADCIWILAAPPE-TRIQLQFEDRFDIEVTPN--CTSNYLELRDGVSDS 2289

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QY 117 GSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDYFSEPGFCIHYSI 162
      : : : : : : : : : : : : : : : : : : : : : :
Db 2290 ABILSKFCGT-SLPSSQSSGCVMLRFRSDN-SPTHVGFKAQSI 2333

RESULT 11
T08618
C:Species: Rattus norvegicus (Norway rat)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: T08618
R:Moestrup, S.K.; Kozyraki, R.; Kristiansen, M.; Kayesen, J.H.; Rasmussen, H.H.; Brault,
J. Biol. Chem. 273, 5235-5242, 1998
A:Title: The intrinsic factor-vitamin B12 receptor and target of teratogenic antibodies
A:Reference number: Z16459; MUID:98148073; PMID:9478979
A:Accession: T08618
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-3623 <MOE>
A:Cross-References: UNIPROT:070244; EMBL:AF022247; NID:g3834379; PIDN:AAC71661.1; PID:g3
C:Genetics:
A:Gene: CUBILIN
C:Superfamily: intrinsic factor-B12 receptor cubilin; EGF homology
C:Keywords: egg yolk; endocytosis; glycoprotein; intestine; kidney; peripheral membrane
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-3623/Product: intrinsic factor-B12 receptor CUBILIN #status predicted <MAT>
F:133-164/Domain: EGF homology <EGF>
F:436-467/Domain: EGF homology <EGF>

Query Match 8.7%; Score 160; DB 2; Length 3623;
Best Local Similarity 26.8%; Pred. No. 0.00028;
Matches 90; Conservative 44; Mismatches 130; Indels 72; Gaps 23;

QY 31 QLSSDKEQGVQDPRHREVVTISGNSIHSPKFTYPRNMVLVRLVAVDENVRIQLTF 90
      : : : : : : : : : : : : : : : : : : : : : :
Db 924 KPSDDKLECG-----EVLTA-SGIIESPGHPNYPGRVNCVTHVV-VORGQIRLEF 974

QY 91 DERFGLPEDDICKYDFVEEPEPSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDYF 150
      : : : : : : : : : : : : : : : : : : : : : :
Db 975 SS-FYLEFHYN--CTNDVLEIYDTAAQTLFGRYCGK-SIPPSLTSNSIKLIFVSDSAL 1030

QY 151 PSEPGFCIH-----STIMPOVTT-----TSPSVLP---PSS-----LSLDLNNAVT 191
      : : : : : : : : : : : : : : : : : : : : : :
Db 1031 AHE-GFSINYEAIDASSVCLVYDTDNFGMLSPN-FPNYPSPNWCIVRIITVGLNQIAL 1088

QY 192 AFS--TLSEELRYLEPDRWQVDLSLYKFTWOLLCAPLYGKSKVNLNLLKEEVKLY- 248
      : : : : : : : : : : : : : : : : : : : : : :
Db 1089 HFTDFTLSDYFGSCQVDFVEI-RDGGYE-TSLVVG---IY--CGSVLPPTIISHSNKLWL 1141

QY 249 -----SCTPRNFVSISREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNEQCQVPRKVT 302
      : : : : : : : : : : : : : : : : : : : : : :
Db 1142 KFKSDAALTAKGFS-----YWDGS--STGCGN-----LTPTGVLTSPNTPM 1183

QY 303 KKYHE---VLQLRPTKGVKGLHKSITDVALHHEEC 335
      : : : : : : : : : : : : : : : : : : : : : :
Db 1184 PYTHSSECVWRLEASHG-SPPELEQDFLHHPSC 1218

RESULT 12
A55362
procollagen I C-proteinase enhancer protein precursor - human
C:Species: Homo sapiens (man)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 15-Mar-2004
C:Accession: A55362
R:Itakahara, K.; Kessler, E.; Biniaminov, L.; Brusel, M.; Eddy, R.L.; Jani-Sait, S.; Show
J. Biol. Chem. 269, 26280-26285, 1994
A:Title: Type I procollagen COOH-terminal proteinase enhancer protein: identification, p
A:Reference number: A55362; MUID:95014462; PMID:7523404
A:Accession: A55362
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-449 <TAK>

A:Cross-References: GB:L33799; NID:g642907; PIDN:AAA61949.1; PID:g642908
C:Genetics:
A:Gene: GDB:PCOLCE
A:Cross-References: GDB:305468; OMIM:600270
A:Map position: 7q21.3-7q22
C:Keywords: extracellular protein; glycoprotein; pyroglutamic acid
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-449/Product: #status predicted <MAT>
F:37-146/Domain: C1r/C1s repeat homology <C1r1>
F:159-270/Domain: C1r/C1s repeat homology <C1r2>
F:226/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F:229,431/Binding site: carbohydrate (Aen) #status predicted

Query Match 8.5%; Score 158; DB 2; Length 449;
Best Local Similarity 34.5%; Pred. No. 3e-05;
Matches 48; Conservative 21; Mismatches 50; Indels 20; Gaps 9;

QY 56 GSIHSPKFPHT-YPRNMVLVRLVAVDENVRIQLTFDERFGLPEDDICKYDFVEV--- 111
      : : : : : : : : : : : : : : : : : : : : : :
Db 168 GTLTTPNWPESDYPGIGSCSHHIIAPPDQV-IALTFF-EKFDLE--PDYCYRDSVSVFNG 223

QY 112 EEPDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDYFSEPGFCIHYSIIM----- 164
      : : : : : : : : : : : : : : : : : : : : : :
Db 224 AVSDSRRLGKFCGD-AVPGSISSEGNELLVQFVSDLSVTAD-GFSASYKTLPRGTAKEG 281

QY 165 --PQVTTTSPSV-LPPSS 180
      : : : : : : : : : : : : : : : : : : : : : :
Db 282 QGPGPKRGTEPKVLPPKS 300

RESULT 13
A39288
dorsal-ventral patterning protein tolloid (EC 3.4.24.-) - fruit fly (Drosophila melanoga
C:Species: Drosophila melanogaster
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A39288
R:Shimell, M.J.; Ferguson, E.L.; Childs, S.R.; O'Connor, M.B.
Cell 67, 469-481, 1991
A:Title: The Drosophila dorsal-ventral patterning gene tolloid is related to human bone
A:Reference number: A39288; MUID:92034970; PMID:1840509
A:Accession: A39288
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1057 <SHI>
A:Cross-References: UNIPROT:P25723; GB:M76976; NID:g157305; PIDN:AAA28491.1; PID:g157306
C:Genetics:
A:Gene: FlyBase:tlid
A:Cross-References: FlyBase:FBgn0003719
C:Superfamily: dorsal-ventral patterning protein tolloid; astacin homology; C1r/C1s repe
C:Keywords: duplication; hydrolase; metalloproteinase; zinc
F:136-329/Domain: astacin homology <AST>
F:352-464/Domain: C1r/C1s repeat homology <C1r1>
F:468-578/Domain: C1r/C1s repeat homology <C1r2>
F:585-620/Domain: EGF homology <EG1>
F:624-740/Domain: C1r/C1s repeat homology <C1r3>
F:747-782/Domain: EGF homology <EG2>
F:787-896/Domain: C1r/C1s repeat homology <C1r4>
F:900-1013/Domain: C1r/C1s repeat homology <C1r5>
F:221,225,231,280/Binding site: zinc (His, His, His, Tyr) #status predicted
F:222/Active site: Glu #status predicted

Query Match 8.3%; Score 153; DB 1; Length 1057;
Best Local Similarity 33.3%; Pred. No. 0.00023;
Matches 47; Conservative 28; Mismatches 54; Indels 12; Gaps 7;

QY 13 LAGQRTGTRAESNLSKQLQSSDKQGVQDPRHREV-----VTISGNGSIHSPKFPHTYP 68
      : : : : : : : : : : : : : : : : : : : : : :
Db 432 VSGEVIITQTSRMLLVNVRNAAGYRGFK-ARFEVCGGDLTKDQSIDSPNYPMDYM 490

QY 69 RNMLVRLVAVDENVRIQLTFDERFGLPEDDICKYDFVEVE--PSDGSVLGRWCGS 126
      : : : : : : : : : : : : : : : : : : : : : :
Db 491 PDKECVIRITAPD-NHQVALKF-QSFELE--KHDGCYDFVEIRDGNHSDRLIGRFCDG 546
```

QY 127 GTPGKQTSKGNHIRFVSD 147
Db 547 KLPPNIKT-RSQMVIKRVSD 566

RESULT 14
T30337
polyprotein - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C:Accession: T30337
R:Yang, J.C.; Lindasay, L.L.; Hedrick, J.L.
submitted to the EMBL Data Library, March 1998
A:Description: cDNA cloning of ovocytinase, a chymotrypsin-like protease released from X
A:Reference number: Z20829
A:Accession: T30337
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1524 <YAN>
A:Cross-references: UNIPROT:Q91674; EMBL:U01290; NID:G2981640; PID:G2981641; PIDN:AAC247
C:Superfamily: tryosin related polyprotein; trypsin homology

Query Match 8.0%; Score 147.5; DB 2; Length 1524;
Best Local Similarity 28.7%; Pred. No. 0.001;
Matches 54; Conservative 34; Mismatches 73; Indels 27; Gaps 10;

QY 56 GSIHSPKFPHTYPRNMVLVAVDENVRIOITDERFGLDEPDDICKYDFVEV-BEP 114
Db 439 GMISFNYPDPYPRNLKTCWS-IIIEAPENHIVLKFED-FNVEYGHG--CIYDAVEVYDGA 494
QY 115 SDGVLGRWCGSGTVPGRKTSKGNHIRFVSDYFPPSPGFCIHYSIIMPO-----VT 168
Db 495 BEKQIARLCGY-TLPLPISSPENTMLIRFKTD-MENSYPGKVRKFSFVPEKQKSLPVD 552
QY 169 ETTSPSVLPSPSLSLDLNNA-VTAFSTLEELIRYLEPD-----RMQVDL-----DS 214
Db 553 DPTITSMHLPRALDVCGMAPTQKWLPRIVGGEASPNMWPQVQIFFLRTTHCEGA 612
QY 215 LYKPTWQL 222
Db 613 IISQWIL 620

RESULT 15
A59271
Ra-reactive factor (EC 3.4.21.-) 2 precursor - human
N:Alternate names: mannose binding protein-associated serine proteinase 2 (MASP-2)
C:Species: Homo sapiens (man)
C>Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C:Accession: A59271
R:Thiel, S.; Vorup-Jensen, T.; Stover, C.M.; Schwaebler, W.J.; Loursen, S.B.; Poulsen, K.
Nature 386, 506-510, 1997
A:Title: A second serine protease associated with mannan-binding lectin that activates c
A:Reference number: A59271; MUID:97242412; PMID:9087411
A:Accession: A59271
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-686 <JEN>
A:Cross-references: UNIPROT:O00187; GB:Y09926; NID:G4007626; PIDN:CAA71059.1; PID:G40076
A:Experimental source: tissue liver
A>Note: submitted to GenBank, December 1996
A>Note: parts of this sequence, including the amino end of the mature protein, were dete
C:Genetics:
A:Gene: GDB:MASP2
A:Cross-references: GDB:6071500
A:Map position: lp36.2-lp36.3
C:Superfamily: complement-activating serine proteases C1r/C1s/MASP; C1r/C1s repeat homol
C:Keywords: beta-hydroxyasparagine; complement pathway; duplication; hydrolase; serine P
F1-15/Domain: signal sequence #status predicted <SIG>
F16-444,445-686/Product: Ra-reactive factor 2 #status predicted <MAT>
F19-134/Domain: C1r/C1s repeat homology <C1R1>
F142-180/Domain: EGF homology <EGF>
F184-293/Domain: C1r/C1s repeat homology <C1R2>

F:300-361/Domain: complement factor H repeat homology <PH1>
F:366-430/Domain: complement factor H repeat homology <PH2>
F:445-679/Domain: trypsin homology <TRI>
F:72-90,142-156,152-165,167-180,184-211,241-259,300-348,328-361,366-412,396-430,434-552,5
F:158/Modified site: erythro-beta-hydroxyasparagine (Asn) #status Predicted
F:444-445/Cleavage site: Arg-Ile (autolytic) #status Predicted
F:483,532,633/Active site: His, Asp, Ser #status Predicted

Query Match 7.9%; Score 145.5; DB 1; Length 686;
Best Local Similarity 30.8%; Pred. No. 0.00055;
Matches 33; Conservative 27; Mismatches 42; Indels 5; Gaps 4;

QY 55 NGSIHSPKFPHTYPRNMVLVAVDENVRIOITDERFGLDEPDDICKYDFVEVEEP 114
Db 193 SGELSSPEYPRPYPKLSSCTYS-ISLEEGFSVILDFVESFDVETHPETLCPIYDLKIQ-- 249

QY 115 SDGVLGRWCGSGTVPGRKTSKGNHIRFVSDYFPPSPGFCIHYS 161
Db 250 TDREHGPFCGK-TLPHRIETKSNVTITFTVDE-SGDHTGKIHYT 294

Search completed: September 3, 2005, 19:30:38
Job time : 26.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 3, 2005, 19:09:34 ; Search time 114.5 Seconds
(without alignments)
1542.946 Million cell updates/sec

Title: US-09-818-943-2

Perfect score: 1848

Sequence: 1 MLLGLLLLTALACQRTGT.....DVALEHHBECDVCKGNAGG 345

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_spport.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1848	100.0	345	2 Q9QY71	Q9QY71 m fallottein
2	1846	99.9	345	2 Q8C119	Q8C119 mus musculus
3	1819	98.4	345	2 Q9JHV8	Q9JHV8 mus musculus
4	1801	97.5	345	2 Q9EQX6	Q9EQX6 rattus norv
5	1667	90.2	345	2 Q9UL22	Q9UL22 homo sapien
6	1664	90.0	345	2 Q9NR41	Q9NR41 homo sapien
7	1552	84.0	345	2 Q91946	Q91946 gallus gall
8	1375	74.4	258	2 Q8K429	Q8K429 rattus norv
9	754	40.8	370	2 Q9BQT1	Q9BQT1 rattus norv
10	752	40.7	370	2 Q9GZP0	Q9GZP0 homo sapien
11	750.5	40.6	364	2 Q9BWP5	Q9BWP5 homo sapien
12	746.5	40.4	370	2 Q9Z517	Q9Z517 mus musculus
13	679.5	36.8	300	2 Q6V9H4	Q6V9H4 oryctolagus
14	440.5	23.8	261	2 Q8K2L3	Q8K2L3 mus musculus
15	201	10.9	923	1 NR1P_BRARE	Q8GFX6 brachydanio
16	201	10.9	923	2 Q69DB8	Q69DB8 brachydanio
17	192.5	10.4	691	2 Q57658	Q57658 gallus gall
18	192	10.4	34	2 Q9JUM4	Q9JUM4 mus musculus
19	191	10.3	707	1 BMP1_XENLA	P98070 xenopus lae
20	191	10.3	977	2 Q91925	Q91925 xenopus lae
21	186.5	10.1	871	2 Q6T869	Q6T869 brachydanio
22	186.5	10.1	959	2 Q69DB7	Q69DB7 brachydanio
23	186.5	10.1	959	2 Q6RT22	Q6RT22 brachydanio
24	186.5	10.1	959	2 Q6T870	Q6T870 brachydanio
25	186	10.1	735	2 Q57381	Q57381 xenopus lae
26	186	10.1	735	2 Q66K13	Q66K13 xenopus lae
27	185	10.0	1015	2 Q9Y6L7	Q9Y6L7 homo sapien
28	185	10.0	1078	2 Q9UQ00	Q9UQ00 homo sapien
29	183.5	9.9	928	1 NR1P_XENLA	P28824 xenopus lae
30	183	9.9	1012	2 Q9WVM6	Q9WVM6 mus musculus
31	181.5	9.8	913	2 Q6NUE0	Q6NUE0 xenopus lae

32	181	9.8	241	2 Q9Z135	Q9Z135 rattus norv
33	181	9.8	775	2 Q6P550	Q6P550 mus musculus
34	181	9.8	986	1 BMP1_HUMAN	P13497 homo sapien
35	181	9.8	991	1 BMP1_MOUSE	P98063 mus musculus
36	181	9.8	991	2 Q6NZM2	Q6NZM2 mus musculus
37	176	9.5	538	2 Q6AWA9	Q6AWA9 homo sapien
38	176	9.5	609	2 Q96190	Q96190 homo sapien
39	176	9.5	641	2 Q71SW6	Q71SW6 homo sapien
40	176	9.5	644	2 Q96IHS	Q96IHS homo sapien
41	176	9.5	704	2 Q9H2E1	Q9H2E1 homo sapien
42	176	9.5	906	2 Q6X907	Q6X907 homo sapien
43	176	9.5	923	1 NR1P_HUMAN	O14786 homo sapien
44	176	9.5	923	2 Q86T59	Q86T59 homo sapien
45	175	9.5	923	2 Q68DN3	Q68DN3 homo sapien

ALIGNMENTS

RESULT 1

Q9QY71 PRELIMINARY; PRT; 345 AA.

AC Q9QY71.01-MAY-2000 (Tremblrel. 13, Last sequence update)

DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)

DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)

DE Fallottein (Platelet-derived growth factor C) (Mus musculus adult male

DE cecum cDNA, RIKEN full-length enriched library, clone:9130403008

DE product:platelet-derived growth factor, C polypeptide, full insert

DE sequence) (Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-

DE length enriched library, clone:A730022G11 product:platelet-derived

DE growth factor, C polypeptide, full insert sequence) (Mus musculus 15

DE days embryo head cDNA, RIKEN full-length enriched library,

DE clone:D930001M08 product:platelet-derived growth factor, C

DE polypeptide, full insert sequence).

GN Name=pfgrfc;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_taxID=10090;

RA [1] TISSUE=Ovary;

RP SEQUENCE FROM N.A.

RC TISSUE=Ovary;

RA Tsai Y.-J., Lee R.K.-K., Chen Y.-H., Lin S.-P., Cheng W.T.-K.;

RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.

EN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J;

RA Gao Z., Hart C., Piddington C., Sheppard P., Shoemaker K.,

RL Gilbertson D., West J., O'Hara P.J.;

RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.

EN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J;

RA TISSUE=Cecum, Cerebellum, and Head;

RL MEDLINE=92979253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;

EN Carninci P., Hayashizaki Y.;

RL "High-efficiency full-length cDNA cloning.;"

RL Meth. Enzymol. 303:19-44(1999).

EN [4]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J;

RA TISSUE=Cecum, Cerebellum, and Head;

RL MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

EN RIKEN FANTOM Consortium;

RL "Functional annotation of a full-length mouse cDNA collection.;"

RL Nature 409:685-690(2001).

EN [5]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J;

RA TISSUE=Cecum, Cerebellum, and Head;

RL The FANTOM Consortium;

RA the RIKEN Genome Exploration Research Group Phase I & II Team;

RL "Analysis of the mouse transcriptome based on functional annotation of

RL 60,770 full-length cDNAs.;"

RL Nature 420:563-573(2002).

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RN RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cecum, Cerebellum, and Head;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata K., Hayatsu M., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RL prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[7]
RN RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cecum, Cerebellum, and Head;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsumai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (KISA) system-384-format
RL sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[8]
RN RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cecum, Cerebellum, and Head;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu M., Hiramoto K., Hiraoka T., Kasukawa T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBSJ databases.
CC -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
DR EMBL; AF17608; AAF22516.1; -.
DR EMBL; AF266467; AAK58566.1; -.
DR EMBL; AK033734; BAC28455.1; -.
DR EMBL; AK042767; BAC31358.1; -.
DR EMBL; AK052947; BAC35216.1; -.
DR HSSP; Q9JJS8; INT0.
DR MGD; MGI:1859631; Pdgfc.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0005161; F:platelet-derived growth factor receptor bin. . .; IDA.
DR GO; GO:0008284; P:positive regulation of cell proliferation; IDA.
DR GO; GO:0050730; P:regulation of peptidyl-tyrosine phosphoryla. . .; IDA.
DR GO; GO:0007171; P:transmembrane receptor protein tyrosine kin. . .; IDA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00341; PDGF; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF 2; 1.
SQ Growth factor; Micogen.
SQ SEQUENCE 345 AA; 38741 MW; 3A58A1F701B84EA2 CRC64;
Query Match 100.0%; Score 1848; DB 2; Length 345;
Best Local Similarity 100.0%; Pred. No. 2.1e-141;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGLLLTSLAGORTCTRAESNLSSKLQLSSQKQNGVQDPRHVRVVTISGNGSIHS 60
DB 1 MLLGLLLTSLAGORTCTRAESNLSSKLQLSSQKQNGVQDPRHVRVVTISGNGSIHS 60
QY 61 PKFPHYTPRNWLVRLVAVDENVRIQLTFDGRFGLGDEDDICKYDFVEVEPSDGSVL 120
DB 61 PKFPHYTPRNWLVRLVAVDENVRIQLTFDGRFGLGDEDDICKYDFVEVEPSDGSVL 120
QY 121 GRWCGSGTVPCKQTSKGNHRIIRFVSDSEYFPSEPGFCIHYSIIIMPOVTTTSPSVLPSS 180
DB 121 GRWCGSGTVPCKQTSKGNHRIIRFVSDSEYFPSEPGFCIHYSIIIMPOVTTTSPSVLPSS 180
QY 181 LSLDLLNNAVTAFTSTLEELIRYLEPDRQVQVLDLSLYKPTWQLLGKAFLYGKSKVNLNL 240
DB 181 LSLDLLNNAVTAFTSTLEELIRYLEPDRQVQVLDLSLYKPTWQLLGKAFLYGKSKVNLNL 240
QY 241 LKBEVKLYSCTPRNFSVSIREELKRTDTIFWPGLLVKRCGNCACCLHNCNEQCQVPRK 300
DB 241 LKBEVKLYSCTPRNFSVSIREELKRTDTIFWPGLLVKRCGNCACCLHNCNEQCQVPRK 300
QY 301 VTKKYHEVLQRPKTVKGLKLSLTDVALEHHEBCDCVCRNAGG 345
DB 301 VTKKYHEVLQRPKTVKGLKLSLTDVALEHHEBCDCVCRNAGG 345
RESULT 2
ID Q8CII19 PRELIMINARY; PRT; 345 AA.
AC Q8CII19;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Platelet-derived growth factor, C polypeptide.
GN Name=pgdfc;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBSJ databases.
CC -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
DR EMBL; BC037696; AAH37696.1; -.
DR HSSP; Q9JJS8; INT0.
DR MGD; MGI:1859631; Pdgfc.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0005161; F:platelet-derived growth factor receptor bin. . .; IDA.
DR GO; GO:0008284; P:positive regulation of cell proliferation; IDA.
DR GO; GO:0050730; P:regulation of peptidyl-tyrosine phosphoryla. . .; IDA.
DR GO; GO:0007171; P:transmembrane receptor protein tyrosine kin. . .; IDA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00341; PDGF; 1.
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DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF_2; 1.
KW Growth factor; Mitogen.
SQ SEQUENCE 345 AA; 38741 MW; 9A58A05C6C0E9614 CRC64;

Query Match 99.9%; Score 1846; DB 2; Length 345;
Best Local Similarity 99.7%; Pred. No. 3e-141;
Matches 344; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLTSALAGORTGTRAESNLSSKQLSSDKQNGVODPRHVRVTTISNGSITHS 60
DB 1 MLLGLLLTSALAGORTGTRAESNLSSKQLSSDKQNGVODPRHVRVTTISNGSITHS 60
QY 61 PKFPHYPRNMVLRVAVDENVRVQLTDFRFGLEDPEDDICKYDFVEVEEPSDGSVL 120
DB 61 PKFPHYPRNMVLRVAVDENVRVQLTDFRFGLEDPEDDICKYDFVEVEEPSDGSVL 120
QY 121 GRWCSGTVPGKQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
DB 121 GRWCSGTVPGKQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
QY 181 LSLDLLNNAVAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLGKAFLYGKSKVVNLNL 240
DB 181 LSLDLLNNAVAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLGKAFLYGKSKVVNLNL 240
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECOCVPRK 300
DB 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECOCVPRK 300
QY 301 VTKKYHEVLQRPKTVGKGLHKSITDVALEHHEECDCVCRNAGG 345
DB 301 VTKKYHEVLQRPKTVGKGLHKSITDVALEHHEECDCVCRNAGG 345

RESULT 3
ID Q9JHV8 PRELIMINARY; PRT; 345 AA.
AC Q9JHV8;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Platelet-derived growth factor C.
GN Name=PDGfc;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss-Webster/NIH;
RX MEDLINE=20417814; PubMed=10960785; DOI=10.1016/S0925-4773(00)00425-1;
RA Ding H., Wu X., Kim I., Tam P.P.L., Koh G.Y., Nagy A.;
RT "The mouse pdgfc gene: dynamic expression in embryonic tissues during organogenesis.";
RL Mech. Dev. 96:209-213(2000).
DR EMBL; AF286725; AAF91483.1; -.
DR HSP; Q9JJS8; INTO.
DR MGD; MGI:1859631; Pdgc.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0005161; P:platelet-derived growth factor receptor bin. . .; IDA.
DR GO; GO:0008284; P:positive regulation of cell proliferation; IDA.
DR GO; GO:0050730; P:regulation of peptidyl-tyrosine phosphoryla. . .; IDA.
DR GO; GO:0007171; P:transmembrane receptor protein tyrosine kin. . .; IDA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF_2; 1.
SQ SEQUENCE 345 AA; 38886 MW; FA1486BED6D362F8 CRC64;

Query Match 97.5%; Score 1801; DB 2; Length 345;
Best Local Similarity 96.8%; Pred. No. 1.3e-137;
Matches 334; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 MLLGLLLTSALAGORTGTRAESNLSSKQLSSDKQNGVODPRHVRVTTISNGSITHS 60
DB 1 MLLGLLLTSALAGORTGTRAESNLSSKQLSSDKQNGVODPRHVRVTTISNGSITHS 60
QY 61 PKFPHYPRNMVLRVAVDENVRVQLTDFRFGLEDPEDDICKYDFVEVEEPSDGSVL 120
DB 61 PKFPHYPRNMVLRVAVDENVRVQLTDFRFGLEDPEDDICKYDFVEVEEPSDGSVL 120
QY 121 GRWCSGTVPGKQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
DB 121 GRWCSGTVPGKQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
QY 181 LSLDLLNNAVAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLGKAFLYGKSKVVNLNL 240
DB 181 LSLDLLNNAVAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLGKAFLYGKSKVVNLNL 240
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECOCVPRK 300
DB 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECOCVPRK 300
QY 301 VTKKYHEVLQRPKTVGKGLHKSITDVALEHHEECDCVCRNAGG 345
DB 301 VTKKYHEVLQRPKTVGKGLHKSITDVALEHHEECDCVCRNAGG 345

RESULT 4
Q9EQX6
ID Q9EQX6 PRELIMINARY; PRT; 345 AA.
AC Q9EQX6;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Spinal cord-derived growth factor.
GN Name=rScdgl;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Kidney;
RX MEDLINE=21092670; PubMed=11162582; DOI=10.1006/bbrc.2000.4187;
RA Hanada T., Ui-Tel K., Imaki J., Miyata Y.;
RT "Molecular cloning of SCDGF-B, a novel growth factor homologous to SCDGF/PDGF-C/fallotain.";
RL Biochem. Biophys. Res. Commun. 280:733-737(2001).
CC -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
DR EMBL; AB033830; BAB19969.1; -.
DR HSP; Q9QJ58; INTO.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008283; P:cell proliferation; IEA.
DR GO; GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00341; PDGF; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF_2; 1.
DR Growth factor; Mitogen.
SQ SEQUENCE 345 AA; 38734 MW; F296DA6E9B765D10 CRC64;

Query Match 97.5%; Score 1801; DB 2; Length 345;
Best Local Similarity 96.8%; Pred. No. 1.3e-137;
Matches 334; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
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QY 1 MLLGLLLLTALAGORTGTRAESNLSSKLQSSDKQNGVDPHRRVVTISNGSIHS 60
DB 1 MLLGLLLLTALAGORTGTRAESNLSSKLQSSDKQNGVDPHRRVVTISNGSIHS 60
QY 61 PKPHTYPRNMVLRVAVDENVRIOITFDRFGLEDPEDDICKYDFVEVEEPSDGSVL 120
DB 61 PKPHTYPRNMVLRVAVDENVRIOITFDRFGLEDPEDDICKYDFVEVEEPSDGSVL 120
QY 121 GRWCSGTVPGKQTSKGNHRIIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPVLPPSS 180
DB 121 GRWCSGTVPGKQTSKGNHRIIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPVLPPSS 180
QY 181 LSLDLLNNAVTAFSTLEELIRYLEPDRMVDLSIKPTWOLGKAFLYGKSKVNLNL 240
DB 181 LSLDLLNNAVTAFSTLEELIRYLEPDRMVDLSIKPTWOLGKAFLYGKSKVNLNL 240
QY 241 LKEEVKLYSCTPRNFSVSIRELKRDTTIFWPGCLLVKRCGNCACCLHNCNECCVPRK 300
DB 241 LKEEVKLYSCTPRNFSVSIRELKRDTTIFWPGCLLVKRCGNCACCLHNCNECCVPRK 300
QY 301 VTKKYHEVLQRLPKTVGKGLHLSLTDVALEHHEECDCVCRGNAGG 345
DB 301 VTKKYHEVLQRLPKTVGKGLHLSLTDVALEHHEECDCVCRGNAGG 345
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RESULT 5
Q9UL22 PRELIMINARY; PRT; 345 AA.
AC Q9UL22;
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
DT 05-JUL-2004 (TremBLrel. 27, Last annotation update)
DE Secretory growth factor-like protein fallotenein (Spinal cord-derived
DE growth factor) (Platelet-derived growth factor C) (VEGF-E).
GN Name=hsCDGF; Synonyms=PDGFC; ORFNames=UNQ174;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RX MEDLINE=20461776; PubMed=11004490; DOI=10.1016/S0167-4781(00)00066-X;
RA Tsai Y.J., Lee R.K., Lin S.P., Chen Y.H.;
RT "Identification of a novel platelet-derived growth factor-like gene,
RT fallotenein, in the human reproductive tract.";
RL Biochim. Biophys. Acta 1492:196-202(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=20317014; PubMed=10858496; DOI=10.1016/S0014-5793(00)01640-9;
RA Hamada T., Ui-Rei K., Miyata Y.;
RT "A novel gene derived from developing spinal cords, SCDGF, is a unique
RT member of the PDGF/VEGF family.";
RL FEBS Lett. 475:97-102(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21347863; PubMed=11297552; DOI=10.1074/jbc.M101056200;
RA Gilbertson D.G., Duff M.E., West J.W., Kelly J.D., Sheppard P.O.,
RA Hofstrand P.D., Gao Z., Shoemaker K., Bukowski T.R., Moore M.,
RA Feldhaus A.L., Humes J.M., Palmer T.E., Hart C.E.;
RT "Platelet-derived growth factor C (PDGF-C), a novel growth factor that
RT binds to PDGF alpha and beta receptor.";
RL J. Biol. Chem. 276:27406-27414(2001).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hase P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
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RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AF091434; AAF00049.1; -
DR EMBL; AB033831; BAB03266.1; -
DR EMBL; AF260738; AAKS1637.1; -
DR EMBL; AY358493; AAQ88857.1; -
DR HSSP; Q9JJS8; 1INT0.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0008083; F:growth factor activity; TAS.
DR GO; GO:0007417; P:central nervous system development; TAS.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00341; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS02078; PDGF_2; 1.
SQ SEQUENCE 345 AA; 39029 MW; CDE9BS1F40633E78 CRC64;

Query Match 90.2%; Score 1667; DB 2; Length 345;
Best Local Similarity 87.0%; Pred. No. 9.6e-127;
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLLGLLLLTALAGORTGTRAESNLSSKLQSSDKQNGVDPHRRVVTISNGSIHS 60
DB 1 MSLFGLLLLTALAGORQTOAESNLSSKFQSSNKQNGVDPQHERIITVSTNGSIHS 60
QY 61 PKPHTYPRNMVLRVAVDENVRIOITFDRFGLEDPEDDICKYDFVEVEEPSDGSVL 120
DB 61 PRFHTYPRNTVLRVAVDENVRIOITFDRFGLEDPEDDICKYDFVEVEEPSDGSVL 120
QY 121 GRWCSGTVPGKQTSKGNHRIIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPVLPPSS 180
DB 121 GRWCSGTVPGKQTSKGNHRIIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPVLPPSS 180
QY 181 LSLDLLNNAVTAFSTLEELIRYLEPDRMVDLSIKPTWOLGKAFLYGKSKVNLNL 240
DB 181 LPLDLLNNAITAFSTLEDLIRYLEPERWQLEDLYRFTWOLGKAFYGRKSRVVDLNL 240
QY 241 LKEEVKLYSCTPRNFSVSIRELKRDTTIFWPGCLLVKRCGNCACCLHNCNECCVPRK 300
DB 241 LTEEVRVLYSCTPRNFSVSIRELKRDTTIFWPGCLLVKRCGNCACCLHNCNECCVPSK 300
QY 301 VTKKYHEVLQRLPKTVGKGLHLSLTDVALEHHEECDCVCRGNAGG 345
DB 301 VTKKYHEVLQRLPKTVGKGLHLSLTDVALEHHEECDCVCRGSTGG 345

RESULT 6
Q9NRA1 PRELIMINARY; PRT; 345 AA.
AC Q9NRA1;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Platelet-derived growth factor C.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=20268201; PubMed=10806482; DOI=10.1038/35010579;
RA Li X., Ponten A., Aase K., Karlsson L., Abramsson A., Uutela M.,
RA Backstrom G., Hellstrom M., Bostrom H., Li H., Soriano P.,
RA Betscholtz C., Heldin C.-H., Allitalo K., Ostman K., Eriksson U.;
RT "PDGF-C is a new protease-activated ligand for the PDGF alpha-
RT receptor.";
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RL Nat. Cell Biol. 2:302-309(2000).
CC -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
DR EMBL; AF244813; AAF80597.1; -.
DR HSSP; Q9JJS8; 1NT0.
DR Genew; HGNC:8801; PDGFC.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008283; P:cell proliferation; IEA.
DR GO; GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF_2; 1.
KW Growth factor; Mitogen.
SQ SEQUENCE 345 AA; 590889CEA55CC5EA CRC64;

Query Match 90.0%; Score 1664; DB 2; Length 345;
Best Local Similarity 86.7%; Pred. No. 1.7e-126;
Matches 299; Conservative 28; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLLGLLLLTALAGQRTGTRAESNLSSKQLSSDKQNGVQDPRHERVVTISNGSIHS 60
Db 1 MSLFGLLLVTSALAGQRRGTQAESNLSSKFPQFSNNKEQNGVQDPQHEKIIITVSTNGSIHS 60
QY 61 PKPHTYPRNMLVRLVAVDENVRIQLTFDRFGLDEPDDICKYDFVEVEEPSDGVTL 120
Db 61 PRPHTYPRNTVLVRLVAVDENVMIQLTFDRFGLDEPDDICKYDFVEVEEPSDGVTL 120
QY 121 GRWCSGTVPGKQTSKGNHIRIRFVSDYFSPGFCIHYSIIMPQVTTTSPSLPPSS 180
Db 121 GRWCSGTVPGKQISKGNQIRIRFVSDYFSPGFCIHYNIVMQFTFVSPSLPPSA 180
QY 181 LSLDLLNNAVAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLLKAFLYGKSKVNLNL 240
Db 181 LPDLNNAITAFSTLEELIRYLEPERWQVLDLEDLYRPTWQLLKAFVFGKRSRVVDNL 240
QY 241 LKEEVLYSCTPRNFSVSIREELKRTDTIFWPGLLVKRCGNCACCLHNCNCCQVPRK 300
Db 241 LKEEVLYSCTPRNFSVSIREELKRTDTIFWPGLLVKRCGNCACCLHNCNCCQVPSK 300
QY 301 VTKKYHEVLQRLPKTKGVKGLHSLTDVALEHHEEDCDVCRCNAGG 345
Db 301 VTKKYHEVLQRLPKTKGVRLHSLTDVALEHHEEDCDVCRCGSTGG 345

RESULT 7
Q9I946 PRELIMINARY; PRT; 345 AA.
AC Q9I946;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Spinal cord-derived growth factor.
GN Name=SCDGF;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=white leghorn; TISSUE=spinal cord;
RX MEDLINE=20317014; PubMed=10858496; DOI=10.1016/S0014-5793(00)01640-9;
RA Hamada T., Ui-Tei K., Miyata Y.;
RT "A novel gene derived from developing spinal cords, SCDGF, is a unique
RT member of the PDGF/VEGF family.";
RL FEBS Lett. 475:97-102(2000).
CC -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
DR EMBL; AB033829; BAB03265.1; -.

DR HSSP; Q9JJS8; 1NT0.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008283; P:cell proliferation; IEA.
DR GO; GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF_2; 1.
KW Growth factor; Mitogen.
SQ SEQUENCE 345 AA; 38940 MW; 97ACEA992BF5128C CRC64;

Query Match 84.0%; Score 1552; DB 2; Length 345;
Best Local Similarity 80.3%; Pred. No. 2e-117;
Matches 277; Conservative 37; Mismatches 31; Indels 0; Gaps 0;

QY 1 MLLGLLLLTALAGQRTGTRAESNLSSKQLSSDKQNGVQDPRHERVVTISNGSIHS 60
Db 1 MLLGLLLLTALAGRRHGAESDLSSKFSFGKQNGVQDPQHEKIIITVSTNGSIHS 60
QY 61 PKPHTYPRNMLVRLVAVDENVRIQLTFDRFGLDEPDDICKYDFVEVEEPSDGVTL 120
Db 61 PKPHTYPRNTVLVRLVAVDENVMIQLTFDRFGLDEPDDICKYDFVEVEEPSDGVTL 120
QY 121 GRWCSGTVPGKQTSKGNHIRIRFVSDYFSPGFCIHYSIIMPQVTTTSPSLPPSS 180
Db 121 GRWCSGTVPRQISKGNQIRIRFVSDYFSPGFCIHLYTLLVPHHTFAPSLSLPPSA 180
QY 181 LSLDLLNNAVAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLLKAFLYGKSKVNLNL 240
Db 181 LPDLNNAVAFSTVLEELIRYLEPDRWQVLDLEDLYRPTWQLLKAFYHGRKSRVDNL 240
QY 241 LKEEVLYSCTPRNFSVSIREELKRTDTIFWPGLLVKRCGNCACCLHNCNCCQVPRK 300
Db 241 LKEEVLYSCTPRNFSVSIREELKRTDTIFWPLCLLVKRCGNCACCHQNCNCCQIPTK 300
QY 301 VTKKYHEVLQRLPKTKGVKGLHSLTDVALEHHEEDCDVCRCNAGG 345
Db 301 VTKKYHEVLQRLPKRSGVRLHSLTDVPLEHHEEDCDVCRCNSEG 345

RESULT 8
Q8K429 PRELIMINARY; PRT; 258 AA.
AC Q8K429;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Platelet-derived growth factor C (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Skin;
RA Brown S.A., Coberly D.M., Rohrich R.R., Chao J.J.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF508348; AAM47265.1; -.
DR HSSP; Q9JJS8; 1NT0.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR PROSITE; PS01180; CUB; 1.
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DR PROSITE; PS50278; PDGF 2; 1.
FT NON_TER 1 1_--
FT NON_TER 258 258
SQ SEQUENCE 258 AA; 29255 MW; 86258989FCC3F8B CRC64;

Query Match 74.4%; Score 1375; DB 2; Length 258;
Best Local Similarity 96.9%; Pred. No. 3.1e-103;
Matches 250; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 42 QDPRHVVTTISGNSIHSKPKPHYPRNMVLVWRLVAVDENVRQLTDFRFGLEDPE 101
Db 1 QDPRHVVTTISGNSIHSKPKPHYPRNTVLVWRLVAVDENVRQLTDFRFGLEDPE 60

QY 102 DICKEYDFVEVEPSPGSLGRWCGSGTVPKQTSKGNHIRIRFVDSVEPSPGFCIHY 161
Db 61 DICKEYDFVEVEPSPGSLGRWCGSGTVPKQTSKGNHIRIRFVDSVEPSPGFCIHY 120

QY 162 LIIMPQVTTTSPVLPPSPSLDLDLNNVAVTAFSTLEELIRLYLEPRWQVLDLSLYKPTW 221
Db 121 LIIMPQVTTTSPVLPPSPSALSLLDLDLNNVAVTAFSTVEELIRLYLEPRWQVLDLSLYKPTW 180

QY 222 LLGKAFLYGKSKAVNLLKKEVLYSCTPRNFSVIREELKRTDTTFWPGCLLVKRCG 281
Db 181 LLGKAFLYGKSKAVNLLKKEVLYSCTPRNFSVIREELKRTDTTFWPGCLLVKRCG 240

QY 282 GNCACCLHNCNCCQVPR 299
Db 241 GNCACCLHNCNCCQVPR 258

RESULT 9
Q9EQT1 PRELIMINARY; PRT; 370 AA.
AC Q9EQT1; 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Spinal-cord derived growth factor-B.
GN Name=rSCDGF-B;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21092670; PubMed=11162582; DOI=10.1006/bbrc.2000.4187;
RA Hamada T., Ui-Tei K., Imaki J., Miyata Y.;
RT "Molecular cloning of SCDGF-B, a novel growth factor homologous to
SCDGF/PDGF-C/fallotain.";
RL Biochem. Biophys. Res. Commun. 280:733-737(2001).
RN EMBL; AB052170; BAB18920.1; -.
DR F01; JC7592; JC7592.
DR HSP; Q9UCV4; INZI.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS50278; PDGF 2; 1.
SQ SEQUENCE 370 AA; 42809 MW; 7BE8A51F679BF73 CRC64;

Query Match 40.8%; Score 754; DB 2; Length 370;
Best Local Similarity 46.2%; Pred. No. 1.1e-52;
Matches 151; Conservative 62; Mismatches 86; Indels 28; Gaps 10;

QY 37 EQNGVQD-PRHREVVTTISGNSIHSKPKPHYPRNMVLVWRLVAVDENVRQLTDFRFG 95
Db 42 ESNHLDLYRRDENIRVTGQVSPRFPNSYPRNLLLTWRLHS-QEKTRIQLAEDHQFG 100

QY 96 LEDPEDDICKYDFVEVEPSPGSLGRWCGSGTVPKQTSKGNHIRIRFVDSVEPSP 153
Db 101 LEEAENDICRYDFVEVEPSPGSLGRWCGSGTVPKQTSKGNHIRIRFVDSVEPSP 160

QY 154 PGFCIHYII--MPQ-----VTET-----TSPSVLPSPSLDLDLNNVAVTAFST 195
Db 161 PGFCIHYISFVDFQPEAAEINWESVTSSPSGVSHPSPVM-DSTLTADALDKAIEPDT 219

QY 196 LEEILRYLEPRWQVLDLSLYKPTWQVLDLSLYKPTWQVLDLSLYKPTWQVLDLSLYKPTW 255
Db 220 VEDLLKYFNPAWQDLENLYMDTPRYGRSY-HERKSK-VDLRLNDVDDVRYSCPTPNH 277

QY 256 SVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNCCQVPRKVTKKYHEVLQLRP-- 313
Db 278 SVNIREELKLTNAVFPFPCLLVQRCGCGGTLNWKSCCTCSSGKTVKKYHEVLKFEPEGH 337

QY 314 -KTGKGLHKLSTVDVALEHHEECDCVC 339
Db 338 FKRRGKAKNMALVDIQLDHHERCDCIC 364

RESULT 10
Q9GZP0 PRELIMINARY; PRT; 370 AA.
AC Q9GZP0; 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Spinal cord-derived growth factor-B (MSP036) (Platelet-derived growth
factor D) (Iris-expressed growth factor long form).
GN Name=hSCDGF-B; Synonyms=IEGF, PDGFD;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21092670; PubMed=11162582; DOI=10.1006/bbrc.2000.4187;
RA Hamada T., Ui-Tei K., Imaki J., Miyata Y.;
RT "Molecular cloning of SCDGF-B, a novel growth factor homologous to
SCDGF/PDGF-C/fallotain.";
RL Biochem. Biophys. Res. Commun. 280:733-737(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Aorta;
RA Liu B., Liu Y.-Q., Wang X.Y., Zhao B., Sheng H., Zhao X.W., Liu S.,
Xu Y.Y., Ye J., Song L., Gao Y., Zhang C.L., Zhang J., Wei Y.J.,
Cao H.Q., Zhao Y., Liu L.S., Ding J.F., Gao R.L., Wu Q.Y., Qiang B.Q.,
Yuan J.G., Liew C.C., Zhao M.S., Hui R.T.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21231380; PubMed=11331882; DOI=10.1038/35074593;
RA LaRoche W.J., Jeffers M., McDonald W.F., Chillaakuru R.A.,
Giese N.A., Lokker N.A., Sullivan C., Boldog F.L., Yang M., Vernet C.,
Burgess C.E., Fernandez E., Deegler L.L., Rittman B., Shimkets J.,
Shimkets R.A., Rothberg J.M., Lichtenstein H.S.;
RT "PDGF-D, A Novel Protease-Activated Growth Factor.";
RL Nat. Cell Biol. 3:517-521(2001).
RN [4]
RP SEQUENCE FROM N.A.
RX PubMed=11331881; DOI=10.1038/35074588;
RA Bergsten E., Untela M., Li X., Pietras K., Ostman A., Heldin C.H.,
Altalio K., Eriksson U.;
RT "PDGF-D is a specific, protease-activated ligand for the PDGF beta-
receptor.";
RL Nat. Cell Biol. 3:512-516(2001).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Iris;
RX MEDLINE=22103462; PubMed=12107412;
RA Wistow G., Berstein S.L., Ray S., Wyatt M.K., Behal A., Touchman J.W.,
Bouffard G., Smith D., Peterson K.;

Db 45 RRETIQKNGYGVSPRPFPNSYPRNLLLTWRHLS-QENTRIQLVFDNQFGLGEAEANDIC 103
Qy 105 KYDVEVEBPSPGSLV--GRWCGSGTVPGKQTSKGNHRIIRVPSDEYPPSPBPGFCIHYSI 162
Db 104 RIDFVEVEDISTSTIIRGRWGHKEVPPRIKSRINQIKITPKSDYFVAKPFGKIYISL 163
Qy 163 I---MPQVTETT-----SPSVLPSPSLDLNNAVTAFTLEELIRYLE 204
Db 164 LEDFQPAASSETNWESVTSISSGVSNPSVTDPT-LTIADALDKKIAEFTDVEDLLKYFN 222
Qy 205 PRRWQVLDLSKYPTWQLLKGAFLYGKSKSVNMLNLLKEVKLYSCTPRNFSVSIREELK 264
Db 223 PESWQEDLENMYLDTPRYRGRSY-HDRKSK-VDLDRLNDDAKRYSCCTPRNYSVNIREEBK 280
Qy 265 RTDTIFPWCGLLVKRCGNCACCLHNCNECCQCPKPKVKKVHEVLQLRP---KTGVKGLH 321
Db 281 LANVFFPRCLLVQRCGNGCGTWNRSCTNSGKTWKVKKVHEVLQFPFGHKKRRGRANT 340
Qy 322 KSLTDVALEHHEBCDVC 339
Db 341 MALVDIQLDHHERCDCIC 358

RESULT 12
Q92517
ID Q92517 PRELIMINARY; PRT; 370 AA.
AC Q92517; Q9D1L8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Platelet-derived growth factor D (Mus musculus 18-day embryo whole
body cDNA, RIKEN full-length enriched library, clone:1110003109
DE product:platelet-derived growth factor D).
GN Name:Pdgfrd;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=BA1B/c;
RX MEDLINE=21231380; PubMed=11331882; DOI=10.1038/35074593;
RA LaRocheWelle W.J., Jeffers M., McDonald W.F., ChillaKuru R.A.,
RA Giese N.A., Lokker N.A., Sullivan C., Boldog F.L., Yang M., Vernet C.,
RA Burgess C.E., Fernandez E., Desglers L.L., Rittman B., Shinkets J.,
RA Shinkets R.A., Rothberg J.M., Lichenstein H.S.;
RT "PDGFR D, A Novel Protease-Activated Growth Factor";
RL Nat. Cell Biol. 3:517-521(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;

REX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagao K., Nagao K., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Tozawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RA Arachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito K., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF335583; AAK38839.1; -
DR EMBL; AK003359; BAB22735.2; -
DR HSSP; Q9JUS8; 1NT0.
DR MGD; MGI:1919035; Pdgfr.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0050730; P:regulation of peptidyl-tyrosine phosphoryla. .; IDA.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS02078; PDGF 2; 1.
SQ SEQUENCE 370 AA; 42809 MW; 9E80B4CF6813BFBE CRC64;

Query Match 40.4%; Score 746.5; DB 2; Length 370;
Best Local Similarity 43.5%; Pred. No. 4.3e-52;
Matches 151; Conservative 63; Mismatches 102; Indels 31; Gaps 9;

Qy 16 QRTGTRAESNLSKQLQSSDKXQGVQDPRIHVVITSGNHSIHPKPHYPRNVLVW 75
Db 26 QRASIKALRNAN---LRRDESNHLTDLYQREENITQVTSNGHVSPSPFPNPRLLLTW 81
Qy 76 RLVAVDENVRIQLTDFERFGLDEDDICDKDFVEVEBPSPDGS--VLGRWCGSGTVPGKQ 133
Db 82 WLRS--QEKTRIQLSPDHFQGLGEAEANDICRYDFVEVEBPSPDGSVTVVRGRWCGHKEIPPRI 140
Qy 134 TSKGNHRIIRFVSPDEYFPSPBPGFCIHYSII---MPQVTETT-----SPSV 175
Db 141 TSRTNQIKITPKSDYFVAKPFGKIYISYFVEDFQPEAASETNWESVTSFSGSVSHSPSI 200
Qy 176 LPPSLSLDLNNNAVTAFTLEELIRYLEPDRWQVLDLSLYKPTWQLLKGAFLYGKSKV 235
Db 201 TDP-TLTADALDKTVAEPDITVEDLLKHFNPSVQDDLENLYLDTPHYRGRSY-HDRKSK- 257
Qy 236 VNALLKEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCSCQ 295
Db 258 VDLORLNDVVKRYSCCTPRNHSVNLRKEULKLTNAVFFPRCLLVQRCGNGCGTGVNWKSGT 317
Qy 296 CVPRKVTKKYHEVLQLRP---KTGVKGLHLSLTDVALEHHEBCDVC 339

Db 318 CSSGKTVKKYHEVLPEPGHFKRGGKAKNMALVDIQLDHHRCDCIC 364

RESULT 13

Q6V9H4 PRELIMINARY; PRT; 300 AA.
AC Q6V9H4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
GN Irie-expressed growth factor (Fragment).
Name=PDGf;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Ray S., Wistow G.
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY347260; AAQ24382.1; -
DR GO; GO:0016020; C-membrane; IEA.
DR GO; GO:0008083; F-growth factor activity; IEA.
DR GO; GO:0008151; P-cell growth and/or maintenance; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PDG_2; 1.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF_2; 1.
FT NON_TER 1
FT NON_TER 300 300
SQ SEQUENCE 300 AA; 34616 MW; 716C873C9C01C0C6 CRC64;

Query Match 36.8%; Score 679.5; DB 2; Length 300;
Best Local Similarity 44.6%; Pred. No. 9e-47;
Matches 135; Conservative 58; Mismatches 83; Indels 27; Gaps 8;
QY 52 ISGSIHSPKPHPTYPNNMLVLRVAVDENVRITQLTFDERFGLDEDDICKYDFVEV 111
Db 2 VTGNHGVQSLAFNSIPRNLTLTWLHLS--QETRIQLAFDHQGLEEAENDICRYDFVEV 60
QY 112 BEPSPDGS--VLGRWCSTGTPGKQTSKGNHIRFVDSFEPSPGFCIHYSII---MPQ 166
Db 61 EDISSTSTVIRGWCQGHKEVPPRITRTNQIKITPKSDDYFVAKGFKIYYSFVEDFQA 120
QY 167 VTET-----SPSVLPSSLSLDLNNAVTAFSTLEELIRYLEPDRQVD 211
Db 121 AASSTNWSVTSISGVSYHNPSTDP--TLTADALDKTIAEFTVEDLLKHPNPSQWBD 179
QY 212 LBSLYKPTWQLLKGAFYCKKSKVNNLILKEEVKLYCTPRNFSVIREELKRTDTIPW 271
Db 180 LENLYLDTPHYGRSY-HDRKSK-VLDRLNDADKRYCTPRNYSVNLREELKTNVVF 237
QY 272 PGLVLRKCGNCACCLHNCPCQCQVPRKVTKKYHEVLQLRP---KTGVKGLHLSITDVA 328
Db 238 PRCLLVQRCGCGCGTGVNWKSTCSSGKTVKKYHEVLKFEFGHFKRRNRAKNMALVDIQ 297
QY 329 LEH 331
Db 298 LDH 300

RESULT 14

Q8K2L3 PRELIMINARY; PRT; 261 AA.
AC Q8K2L3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE PDGf protein.
GN Name=PDGf;

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor; DOI=10.1073/pnas.242603899;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC030896; AAH30896.1; -
DR HSP; Q9JJS8; 1NT0.
DR MGD; MGI:1919035; Pdgfd.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0050730; P:regulation of peptidyl-tyrosine phosphoryla. .; IDA.
DR InterPro; IPR000859; CUB.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF_2; 1.
SQ SEQUENCE 261 AA; 30228 MW; 2EEC3F6373A52D09 CRC64;
Query Match 23.8%; Score 440.5; DB 2; Length 261;
Best Local Similarity 38.7%; Pred. No. 1.8e-27;
Matches 94; Conservative 49; Mismatches 73; Indels 27; Gaps 7;
QY 16 QRTGTRASNLSSKLQSSDKQNGVQDPHRRVVTISNGSIHSPKPHPTYPNNMLVW 75
Db 26 QRASIKALRNAN---LRDESNHLTLQYREENIQVTSNGHVQSPFPNSYPRNLLTW 81
QY 76 RLVAVDENVRITQLTFDERFGLDEDDICKYDFVEVEEPPSDGS--VLGRWCSTGTPGKQ 133
Db 82 WLRS--QETRIQLGFDHGFGLAEAAENDICRYDFVEVEEVSSTTVVRGRCWGHKEIPRI 140
QY 134 TSKGNHIRFVDSFEPSPGFCIHYSII---NPQVTETT-----SPSV 175
Db 141 TSRTNQIKITPKSDDYFVAKGFKIYYSFVEDSQEPAASETNWESVTSFSGVSHSPSI 200
QY 176 LPSSLSLDLNNAVTAFSTLEELIRYLEPDRQVDLSLYKPTWQLLKGAFYCKKSKV 235
Db 201 TDP--TLTADALDKTVAEFTVEDLLKHPNPSQWQDLENLYLDTPHYGRSY-HDRKSKG 258
QY 236 VNL 238
Db 259 IEV 261
RESULT 15
NRPI BRARE
ID NRPI_BRARE STANDARD; PRT; 923 AA.
AC Q8QFX6; Q8AXP1;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 3, 2005, 19:19:05 ; Search time 30 Seconds
(without alignments)
858.464 Million cell updates/sec

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Perfect score: 1848
Sequence: 1 MLLGLLLLTSAAGQRTGT.....DVALEHHECDVCVRGNAGG 345

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1848	100.0	345	US-09-457-066-43	Sequence 43, Appl
2	1848	100.0	345	US-09-564-595D-35	Sequence 35, Appl
3	1848	100.0	345	US-09-706-968-43	Sequence 43, Appl
4	1848	100.0	345	US-09-823-033-4	Sequence 4, Appl
5	1848	100.0	345	US-10-139-583-43	Sequence 43, Appl
6	1667	90.2	345	US-09-040-220D-2	Sequence 2, Appl
7	1667	90.2	345	US-09-457-066-2	Sequence 2, Appl
8	1667	90.2	345	US-09-265-686-2	Sequence 2, Appl
9	1667	90.2	345	US-09-540-224-5	Sequence 5, Appl
10	1667	90.2	345	US-09-564-595D-33	Sequence 33, Appl
11	1667	90.2	345	US-09-706-968-2	Sequence 110, Appl
12	1667	90.2	345	US-09-723-749-2	Sequence 2, Appl
13	1667	90.2	345	US-09-823-033-2	Sequence 2, Appl
14	1667	90.2	345	US-09-468-647A-101	Sequence 101, Appl
15	1667	90.2	345	US-09-468-647A-110	Sequence 110, Appl
16	1667	90.2	345	US-09-468-647A-130	Sequence 130, Appl
17	1667	90.2	345	US-10-139-583-2	Sequence 2, Appl
18	1667	90.2	374	US-09-468-647A-118	Sequence 118, Appl
19	1659	89.8	345	US-09-468-647A-2	Sequence 2, Appl
20	1659	89.8	345	US-09-468-647A-103	Sequence 103, Appl
21	1586	85.8	354	US-09-468-647A-120	Sequence 120, Appl
22	1586	85.8	355	US-09-468-647A-122	Sequence 122, Appl
23	1578	85.4	323	US-09-468-647A-1	Sequence 1, Appl
24	1267.5	68.6	282	US-09-468-647A-112	Sequence 112, Appl
25	1204.5	65.2	303	US-09-564-595D-57	Sequence 57, Appl
26	1200	64.9	302	US-09-564-595D-54	Sequence 54, Appl
27	1035.5	56.0	317	US-09-564-595D-56	Sequence 56, Appl

28	1019	55.1	316	4	US-09-564-595D-55	Sequence 55, Appl
29	752	40.7	370	4	US-09-457-066-37	Sequence 37, Appl
30	752	40.7	370	4	US-09-540-224-2	Sequence 2, Appl
31	752	40.7	370	4	US-09-564-595D-2	Sequence 2, Appl
32	752	40.7	370	4	US-09-706-968-37	Sequence 37, Appl
33	752	40.7	370	4	US-09-808-372-2	Sequence 2, Appl
34	752	40.7	370	4	US-09-823-033-5	Sequence 5, Appl
35	752	40.7	370	4	US-09-438-046-8	Sequence 8, Appl
36	752	40.7	370	4	US-10-139-583-37	Sequence 37, Appl
37	752	40.7	370	4	US-10-039-847A-2	Sequence 2, Appl
38	750.5	40.6	322	4	US-09-438-046-6	Sequence 6, Appl
39	746.5	40.4	370	4	US-09-540-224-4	Sequence 4, Appl
40	746.5	40.4	370	4	US-09-564-595D-53	Sequence 53, Appl
41	746.5	40.4	370	4	US-09-808-972-4	Sequence 4, Appl
42	746.5	40.4	370	4	US-10-039-847A-4	Sequence 4, Appl
43	720	39.0	167	4	US-09-468-647A-111	Sequence 111, Appl
44	713	38.6	168	4	US-09-468-647A-27	Sequence 27, Appl
45	713	38.6	168	4	US-09-468-647A-126	Sequence 126, Appl

ALIGNMENTS

RESULT 1
US-09-457-066-43
; Sequence 43, Application US/09457066
; Patent No. 6432673
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/09/457,066
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-457-066-43

Query Match		100.0%;	Score 1848;	DB 4;	Length 345;
Best Local Similarity		100.0%;	Pred. No. 8.2e-195;		
Matches 345;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MLLGLLLLTSAAGQRTGTRAESNLSSKLQSSDKQNGVQDPRHVRVVTISGNSIHS	60		
Db	1	MLLGLLLLTSAAGQRTGTRAESNLSSKLQSSDKQNGVQDPRHVRVVTISGNSIHS	60		
Qy	61	PKPHTYPRNNVLVRLVAVDENVRIQLTFDERFGLDEPDIDICKYDFVEVEEPSDGSVL	120		
Db	61	PKPHTYPRNNVLVRLVAVDENVRIQLTFDERFGLDEPDIDICKYDFVEVEEPSDGSVL	120		
Qy	121	GRWCGSTVPGKQTSKGNHRIKRVSDYEPFSEPGFCHYHSIIMPQVTTTSPSVLPSS	180		
Db	121	GRWCGSTVPGKQTSKGNHRIKRVSDYEPFSEPGFCHYHSIIMPQVTTTSPSVLPSS	180		
Qy	181	LSLDLNNVATFSTLEELRYLEPDRQVLDLSLYKPTWQLLKAFLYGKKSKVNNLNL	240		
Db	181	LSLDLNNVATFSTLEELRYLEPDRQVLDLSLYKPTWQLLKAFLYGKKSKVNNLNL	240		
Qy	241	LKEEVKLYSCTPRNFVSIRIELKRTDTIIFWPGCLLVKRCGNCACCLHNCNECCQVPRK	300		
Db	241	LKEEVKLYSCTPRNFVSIRIELKRTDTIIFWPGCLLVKRCGNCACCLHNCNECCQVPRK	300		
Qy	301	VTKKYHVLQRPKTVGKGLHSLTUDVALEHHECDVCVRGNAGG	345		
Db	301	VTKKYHVLQRPKTVGKGLHSLTUDVALEHHECDVCVRGNAGG	345		

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Db 301 VTKYHEVLQRLPKTGKGLHKSITDVALEHHEECDCVCRNAGG 345

RESULT 2
US-09-564-595D-35
; Sequence 35, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-564-595D-35

Query Match 100.0%; Score 1848; DB 4; Length 345;
Best Local Similarity 100.0%; Pred. No. 8.2e-195;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLTSALAGQRTGTRAESNLSSKQLSSDKQNGVODPRHVRVTTISNGSIHS 60
Db 1 MLLGLLLTSALAGQRTGTRAESNLSSKQLSSDKQNGVODPRHVRVTTISNGSIHS 60
QY 61 PKFPHYPRNMVLVWRLVAVDENVRIOITFDERFGLDEPDICIKYDFVEVEEPSDGSVL 120
Db 61 PKFPHYPRNMVLVWRLVAVDENVRIOITFDERFGLDEPDICIKYDFVEVEEPSDGSVL 120
QY 121 GRWCGSGTVPKGQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
Db 121 GRWCGSGTVPKGQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
QY 181 LSDDLNNAVTAFSTLEELIRYLEPDRWQVDLSLYKPTWQLLKAFLYGKSKVNNLN 240
Db 181 LSDDLNNAVTAFSTLEELIRYLEPDRWQVDLSLYKPTWQLLKAFLYGKSKVNNLN 240
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
Db 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
QY 301 VTKYHEVLQRLPKTGKGLHKSITDVALEHHEECDCVCRNAGG 345
Db 301 VTKYHEVLQRLPKTGKGLHKSITDVALEHHEECDCVCRNAGG 345

RESULT 4
US-09-823-033-4
; Sequence 4, Application US/09823033
; Patent No. 6663870
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE
; FILE REFERENCE: 00-12
; CURRENT APPLICATION NUMBER: US/09/823,033
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-823-033-4

Query Match 100.0%; Score 1848; DB 4; Length 345;
Best Local Similarity 100.0%; Pred. No. 8.2e-195;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLTSALAGQRTGTRAESNLSSKQLSSDKQNGVODPRHVRVTTISNGSIHS 60
Db 1 MLLGLLLTSALAGQRTGTRAESNLSSKQLSSDKQNGVODPRHVRVTTISNGSIHS 60
QY 61 PKFPHYPRNMVLVWRLVAVDENVRIOITFDERFGLDEPDICIKYDFVEVEEPSDGSVL 120
Db 61 PKFPHYPRNMVLVWRLVAVDENVRIOITFDERFGLDEPDICIKYDFVEVEEPSDGSVL 120
QY 121 GRWCGSGTVPKGQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
Db 121 GRWCGSGTVPKGQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
QY 181 LSDDLNNAVTAFSTLEELIRYLEPDRWQVDLSLYKPTWQLLKAFLYGKSKVNNLN 240
Db 181 LSDDLNNAVTAFSTLEELIRYLEPDRWQVDLSLYKPTWQLLKAFLYGKSKVNNLN 240
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
Db 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
QY 301 VTKYHEVLQRLPKTGKGLHKSITDVALEHHEECDCVCRNAGG 345
Db 301 VTKYHEVLQRLPKTGKGLHKSITDVALEHHEECDCVCRNAGG 345

RESULT 3
US-09-706-968-43
; Sequence 43, Application US/09706968
; Patent No. 6528050
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60C1
; CURRENT APPLICATION NUMBER: US/09/706,968
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Db 121 GWCGSGTVPKGQTSKGNHIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
Qy 181 LSLDLLNNAVAFSTLEELIRYLEPDRWQVDLSLYKPTWQLLKGAFYGGKSKVNNL 240
Db 181 LSLDLLNNAVAFSTLEELIRYLEPDRWQVDLSLYKPTWQLLKGAFYGGKSKVNNL 240
Qy 241 LKEEVLKYSCTPRNFSVSIREBLKRTDTTFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
Db 241 LKEEVLKYSCTPRNFSVSIREBLKRTDTTFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
Qy 301 VTKYHEVLQLRPKTGKGLHKSITDVALEHHEBCDCVCRNAGG 345
Db 301 VTKYHEVLQLRPKTGKGLHKSITDVALEHHEBCDCVCRNAGG 345

RESULT 5

US-10-139-583-43

; Sequence 43, Application US/10139583

; Patent No. 6814965

; GENERAL INFORMATION:

; APPLICANT: Gao, Zeren

; APPLICANT: Hart, Charles E.

; APPLICANT: Piddington, Christopher S.

; APPLICANT: Sheppard, Paul O.

; APPLICANT: Shoemaker, Kimberly E.

; APPLICANT: Gilbertson, Debra G.

; APPLICANT: West, James W.

; TITLE OF INVENTION: GROWTH FACTOR HOMOLOGY ZVEGF3

; FILE REFERENCE: 98-60

; CURRENT APPLICATION NUMBER: US/10/139,583

; CURRENT FILING DATE: 2002-05-02

; PRIOR APPLICATION NUMBER: 09/457,066

; PRIOR FILING DATE: 1999-12-07

; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 43

; TYPE: PRT

; ORGANISM: Mus musculus

US-10-139-583-43

Query Match 100.0%; Score 1848; DB 4; Length 345;
Best Local Similarity 100.0%; Pred. No. 8.2e-195;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLGLLLTTSALAGQRTGTRAESNLSSKQLQSSDKQNGVQDPRHVRVTTISNGSIHS 60
Db 1 MLLGLLLTTSALAGQRTGTRAESNLSSKQLQSSDKQNGVQDPRHVRVTTISNGSIHS 60
Qy 61 PKFPHYPRNMVLRVAVDENVRIOITFDRFGLDEPDDICKYDFVEVEEPSDGSVL 120
Db 61 PKFPHYPRNMVLRVAVDENVRIOITFDRFGLDEPDDICKYDFVEVEEPSDGSVL 120
Qy 121 GWCGSGTVPKGQTSKGNHIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
Db 121 GWCGSGTVPKGQTSKGNHIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
Qy 181 LSLDLLNNAVAFSTLEELIRYLEPDRWQVDLSLYKPTWQLLKGAFYGGKSKVNNL 240
Db 181 LSLDLLNNAVAFSTLEELIRYLEPDRWQVDLSLYKPTWQLLKGAFYGGKSKVNNL 240
Qy 241 LKEEVLKYSCTPRNFSVSIREBLKRTDTTFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
Db 241 LKEEVLKYSCTPRNFSVSIREBLKRTDTTFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
Qy 301 VTKYHEVLQLRPKTGKGLHKSITDVALEHHEBCDCVCRNAGG 345
Db 301 VTKYHEVLQLRPKTGKGLHKSITDVALEHHEBCDCVCRNAGG 345

RESULT 6

US-09-040-220D-2

Query Match 90.2%; Score 1667; DB 4; Length 345;

; Sequence 2, Application US/09040220D
; Patent No. 6391311
; GENERAL INFORMATION:
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Ferrara, Napoleone
; TITLE OF INVENTION: NOVEL POLYPEPTIDES HAVING HOMOLOGY TO VASCULAR
; TITLE OF INVENTION: ENDOTHELIAL CELL GROWTH FACTOR AND BONE MORPHOGENETIC
; TITLE OF INVENTION: PROTEIN 1 AND NUCLEIC ACIDS ENCODING SAME, THEIR USES,
; TITLE OF INVENTION: AND PROCESSES FOR THEIR PRODUCTION
; FILE REFERENCE: P1122
; CURRENT APPLICATION NUMBER: US/09/040,220D
; CURRENT FILING DATE: 1998-03-17
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Human
US-09-040-220D-2

Query Match 90.2%; Score 1667; DB 3; Length 345;
Best Local Similarity 87.0%; Pred. No. 7.4e-175;
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

Qy 1 MLLGLLLTTSALAGQRTGTRAESNLSSKQLQSSDKQNGVQDPRHVRVTTISNGSIHS 60
Db 1 MSLFGLLLTTSALAGQRTGTRAESNLSSKQLQSSDKQNGVQDPRHVRVTTISNGSIHS 60
Qy 61 PKFPHYPRNMVLRVAVDENVRIOITFDRFGLDEPDDICKYDFVEVEEPSDGSVL 120
Db 61 PRFPHYPRNMVLRVAVDENVRIOITFDRFGLDEPDDICKYDFVEVEEPSDGSVL 120
Qy 121 GRWCGSGTVPKGQTSKGNHIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
Db 121 GRWCGSGTVPKGQTSKGNHIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
Qy 181 LSLDLLNNAVAFSTLEELIRYLEPDRWQVDLSLYKPTWQLLKGAFYGGKSKVNNL 240
Db 181 LPLDLLNNAITAFSTLEELIRYLEPDRWQVDLSLYKPTWQLLKGAFYGGKSKVNNL 240
Qy 241 LKEEVLKYSCTPRNFSVSIREBLKRTDTTFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
Db 241 LKEEVLKYSCTPRNFSVSIREBLKRTDTTFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
Qy 301 VTKYHEVLQLRPKTGKGLHKSITDVALEHHEBCDCVCRNAGG 345
Db 301 VTKYHEVLQLRPKTGKGLHKSITDVALEHHEBCDCVCRNAGG 345

RESULT 7

US-09-457-066-2

; Sequence 2, Application US/09457066

; Patent No. 6432673

; GENERAL INFORMATION:

; APPLICANT: Gao, Zeren

; APPLICANT: Hart, Charles E.

; APPLICANT: Piddington, Christopher S.

; APPLICANT: Sheppard, Paul O.

; APPLICANT: Shoemaker, Kimberly E.

; APPLICANT: Gilbertson, Debra G.

; APPLICANT: West, James W.

; TITLE OF INVENTION: GROWTH FACTOR HOMOLOGY ZVEGF3

; FILE REFERENCE: 98-60

; CURRENT APPLICATION NUMBER: US/09/457,066

; CURRENT FILING DATE: 1999-12-07

; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 2

; LENGTH: 345

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-457-066-2

Best Local Similarity 87.0%; Pred. No. 7.4e-175;
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLLGLLLTALAGORTGTRAESNLSSKQLSSDKEQNGVODPRHRVVTISNGSIHS 60
DB 1 MSLFGLLLTALAGORQGTQAESNLSSKFQSSNKEQNGVODPQHERIITVSTNGSIHS 60

QY 61 PKFPHYPRNMVLRVAVDENVRIOITFDRFRGLEDPEDDICKYDFVEEPPSDGSVL 120
DB 61 PRFPHYPRNTVLVRLVAEENVMIOITFDRFRGLEDPEDDICKYDFVEEPPSDGTIL 120

QY 121 GRWCSGTVPGKQTSKGNHIRIRFVSDYFPPSEPGFCHYHSIIMPQVTTTSPSVLPSS 180
DB 121 GRWCSGTVPGKQISKGNQIRIRFVSDYFPPSEPGFCHYINVMQPTFVSPVLPSSA 180

QY 181 LSLDLLNNAVAFSTLEELIRVLEPDRQVODLSLYKPTWQLLKAFLYGKSKVNNLNL 240
DB 181 LPDLNNAITAFSTLEDLIRVLEPERWQDLEDLYRPTWQLLKAFVFGKRSRVVDLNL 240

QY 241 LKEEVKLYSCTPRNFSVSIRELKRDTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
DB 241 LTEEVRLYSCTPRNFSVSIRELKRDTDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300

QY 301 VTKKYHEVLQLRPKTGKGLHKSITDVALEHHEBCDCVCRGNAGG 345
DB 301 VTKKYHEVLQLRPKTGVRGLHKSITDVALEHHEBCDCVCRGSTGG 345

RESULT 8
US-09-265-686-2
Query Match 90.2%; Score 1667; DB 4; Length 345;
Best Local Similarity 87.0%; Pred. No. 7.4e-175;
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

Patent No. 6455283
GENERAL INFORMATION:
APPLICANT: Ferrara, Napoleone
APPLICANT: Kuo, Sophia S.
TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND BMP1
FILE REFERENCE: P1122P2
CURRENT APPLICATION NUMBER: US/09/265,686
PRIOR FILING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: US 09/040,220
PRIOR FILING DATE: 1998-03-17
PRIOR APPLICATION NUMBER: US 09/184,216
PRIOR FILING DATE: 1998-11-02
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 2
LENGTH: 345
TYPE: PRT
ORGANISM: Human
US-09-265-686-2

Query Match 90.2%; Score 1667; DB 4; Length 345;
Best Local Similarity 87.0%; Pred. No. 7.4e-175;
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLLGLLLTALAGORTGTRAESNLSSKQLSSDKEQNGVODPRHRVVTISNGSIHS 60
DB 1 MSLFGLLLTALAGORQGTQAESNLSSKFQSSNKEQNGVODPQHERIITVSTNGSIHS 60

QY 61 PKFPHYPRNMVLRVAVDENVRIOITFDRFRGLEDPEDDICKYDFVEEPPSDGSVL 120
DB 61 PRFPHYPRNTVLVRLVAEENVMIOITFDRFRGLEDPEDDICKYDFVEEPPSDGTIL 120

QY 121 GRWCSGTVPGKQTSKGNHIRIRFVSDYFPPSEPGFCHYHSIIMPQVTTTSPSVLPSS 180
DB 121 GRWCSGTVPGKQISKGNQIRIRFVSDYFPPSEPGFCHYINVMQPTFVSPVLPSSA 180

QY 181 LSLDLLNNAVAFSTLEELIRVLEPDRQVODLSLYKPTWQLLKAFLYGKSKVNNLNL 240
DB 181 LPDLNNAITAFSTLEDLIRVLEPERWQDLEDLYRPTWQLLKAFVFGKRSRVVDLNL 240

QY 241 LKEEVKLYSCTPRNFSVSIRELKRDTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
DB 241 LTEEVRLYSCTPRNFSVSIRELKRDTDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300

QY 301 VTKKYHEVLQLRPKTGKGLHKSITDVALEHHEBCDCVCRGNAGG 345
DB 301 VTKKYHEVLQLRPKTGVRGLHKSITDVALEHHEBCDCVCRGSTGG 345

RESULT 9
US-09-540-224-5
Query Match 90.2%; Score 1667; DB 4; Length 345;
Best Local Similarity 87.0%; Pred. No. 7.4e-175;
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

Sequence 5, Application US/09540224
Patent No. 6468543
GENERAL INFORMATION:
APPLICANT: Gilbertson, Debra G.
APPLICANT: Hart, Charles E.
TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4
FILE REFERENCE: 00-28
CURRENT APPLICATION NUMBER: US/09/540,224
EARLIER FILING DATE: 2000-03-31
EARLIER APPLICATION NUMBER: US 60/180,169
EARLIER FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 5
LENGTH: 345
TYPE: PRT
ORGANISM: Homo sapiens
US-09-540-224-5

Query Match 90.2%; Score 1667; DB 4; Length 345;
Best Local Similarity 87.0%; Pred. No. 7.4e-175;
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLLGLLLTALAGORTGTRAESNLSSKQLSSDKEQNGVODPRHRVVTISNGSIHS 60
DB 1 MSLFGLLLTALAGORQGTQAESNLSSKFQSSNKEQNGVODPQHERIITVSTNGSIHS 60

QY 61 PKFPHYPRNMVLRVAVDENVRIOITFDRFRGLEDPEDDICKYDFVEEPPSDGSVL 120
DB 61 PRFPHYPRNTVLVRLVAEENVMIOITFDRFRGLEDPEDDICKYDFVEEPPSDGTIL 120

QY 121 GRWCSGTVPGKQTSKGNHIRIRFVSDYFPPSEPGFCHYHSIIMPQVTTTSPSVLPSS 180
DB 121 GRWCSGTVPGKQISKGNQIRIRFVSDYFPPSEPGFCHYINVMQPTFVSPVLPSSA 180

QY 181 LSLDLLNNAVAFSTLEELIRVLEPDRQVODLSLYKPTWQLLKAFLYGKSKVNNLNL 240
DB 181 LPDLNNAITAFSTLEDLIRVLEPERWQDLEDLYRPTWQLLKAFVFGKRSRVVDLNL 240

QY 241 LKEEVKLYSCTPRNFSVSIRELKRDTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
DB 241 LTEEVRLYSCTPRNFSVSIRELKRDTDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300

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Query Match 90.2%; Score 1667; DB 4; Length 345;
Best Local Similarity 87.0%; Pred. No. 7.4e-175;
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

Sequence 33, Application US/09564595D
Patent No. 6495668
GENERAL INFORMATION:
APPLICANT: Gilbert, Teresa
APPLICANT: Hart, Charles E.
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
FILE REFERENCE: 99-19
CURRENT APPLICATION NUMBER: US/09/564,595D
CURRENT FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: US 09/304,216
PRIOR FILING DATE: 1999-05-03
PRIOR APPLICATION NUMBER: US 60/164,463
PRIOR FILING DATE: 1999-11-10


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RESULT 13
US-09-823-033-2
; Sequence 2, Application US/09823033
; Patent No. 6663870
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE
; FILE REFERENCE: 00-12
; CURRENT APPLICATION NUMBER: US/09/823,033
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-823-033-2

Query Match          90.2%; Score 1667; DB 4; Length 345;
Best Local Similarity 87.0%; Pred. No. 7.4e-175;
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

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Db 61 PRFPHTYPRNTVLVWRLVAVDENVRILQTLTDFRFGLEDPEDDICKYDFVEVEEPSDGSVL 120
QY 121 GRWCGSGTVPGKQTSKGNHIRIRFVSDSEYFPFSEPGFCIHYNIVMPQFTEAVSPVLPSS 180
Db 121 GRWCGSGTVPGKQTSKGNHIRIRFVSDSEYFPFSEPGFCIHYNIVMPQFTEAVSPVLPSS 180
QY 181 LSLDLLNNAVTAFSTLEELIRYLEPDRMQVDLSLYKPTWQLLKGAFLYGKSKVYNLNL 240
Db 181 LPDLLNNAVTAFSTLEELIRYLEPDRMQVDLSLYKPTWQLLKGAFLYGKSKVYNLNL 240
QY 241 LKEEVLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300
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RESULT 15
US-09-468-647A-110
; Sequence 110, Application US/09468647A
; Patent No. 6783953
; GENERAL INFORMATION:
; APPLICANT: Gordon, Robert D
; APPLICANT: Sprengel, Jorg J
; APPLICANT: Von, Jeffery R
; APPLICANT: Dijkmans, Josiena J.H.
; APPLICANT: Gosiewska, Anna
; APPLICANT: Dhanaraj, Sridevi N
; APPLICANT: Xu, Jean
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-X
; FILE REFERENCE: B0192.70011US00
; CURRENT APPLICATION NUMBER: US/09/468,647A
; CURRENT FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: GB 9828377.3
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: US 60/124,967
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: US 60/164,131
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 110
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-468-647A-110

Query Match          90.2%; Score 1667; DB 4; Length 345;
Best Local Similarity 87.0%; Pred. No. 7.4e-175;
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

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QY 121 GRWCGSGTVPGKQTSKGNHIRIRFVSDSEYFPFSEPGFCIHYNIVMPQFTEAVSPVLPSS 180
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QY 241 LKEEVLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300
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RESULT 14
US-09-468-647A-101
; Sequence 101, Application US/09468647A
; Patent No. 6783953
; GENERAL INFORMATION:
; APPLICANT: Gordon, Robert D
; APPLICANT: Sprengel, Jorg J
; APPLICANT: Von, Jeffery R
; APPLICANT: Dijkmans, Josiena J.H.
; APPLICANT: Gosiewska, Anna
; APPLICANT: Dhanaraj, Sridevi N
; APPLICANT: Xu, Jean
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-X
; FILE REFERENCE: B0192.70011US00
; CURRENT APPLICATION NUMBER: US/09/468,647A
; CURRENT FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: GB 9828377.3
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: US 60/124,967
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: US 60/164,131
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 130
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				
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2	1848	100.0	345	9 US-09-818-943-2 Sequence 2, Appli
3	1848	100.0	345	9 US-09-852-209A-7 Sequence 7, Appli
4	1848	100.0	345	11 US-09-876-813-35 Sequence 35, Appli
5	1848	100.0	345	13 US-10-139-563-43 Sequence 43, Appli
6	1848	100.0	345	14 US-10-131-600-7 Sequence 7, Appli
7	1848	100.0	345	14 US-10-264-361-4 Sequence 4, Appli
8	1848	100.0	345	15 US-10-303-957B-7 Sequence 7, Appli
9	1848	100.0	345	15 US-10-664-432-4 Sequence 4, Appli
10	1848	100.0	345	15 US-10-439-337A-7 Sequence 7, Appli
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12	1848	100.0	345	16	US-10-877-623-35	Sequence 35, Appli
13	1848	100.0	345	17	US-10-938-375-4	Sequence 4, Appli
14	1848	100.0	345	20	US-11-021-088-43	Sequence 43, Appli
15	1848	100.0	345	20	US-11-080-803-35	Sequence 35, Appli
16	1667	90.2	345	9	US-09-823-033-2	Sequence 2, Appli
17	1667	90.2	345	9	US-09-923-935-4	Sequence 4, Appli
18	1667	90.2	345	9	US-09-795-006A-149	Sequence 149, App
19	1667	90.2	345	9	US-09-978-295A-488	Sequence 488, App
20	1667	90.2	345	9	US-09-978-697-488	Sequence 488, App
21	1667	90.2	345	9	US-09-978-192A-488	Sequence 488, App
22	1667	90.2	345	9	US-09-999-832A-488	Sequence 488, App
23	1667	90.2	345	10	US-09-978-189-488	Sequence 488, App
24	1667	90.2	345	10	US-09-796-753-6	Sequence 6, Appli
25	1667	90.2	345	10	US-09-978-608A-488	Sequence 488, App
26	1667	90.2	345	10	US-09-978-585A-488	Sequence 488, App
27	1667	90.2	345	10	US-09-978-191A-488	Sequence 488, App
28	1667	90.2	345	10	US-09-978-403A-488	Sequence 488, App
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30	1667	90.2	345	10	US-09-999-833A-488	Sequence 488, App
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32	1667	90.2	345	10	US-09-978-824-488	Sequence 488, App
33	1667	90.2	345	10	US-09-918-585A-488	Sequence 488, App
34	1667	90.2	345	10	US-09-999-834A-488	Sequence 488, App
35	1667	90.2	345	10	US-09-378-423A-488	Sequence 488, App
36	1667	90.2	345	10	US-09-978-193A-488	Sequence 488, App
37	1667	90.2	345	10	US-09-999-830A-488	Sequence 488, App
38	1667	90.2	345	10	US-09-978-757A-488	Sequence 488, App
39	1667	90.2	345	10	US-09-978-187B-488	Sequence 488, App
40	1667	90.2	345	10	US-09-978-643A-488	Sequence 488, App
41	1667	90.2	345	10	US-09-978-375A-488	Sequence 488, App
42	1667	90.2	345	10	US-09-978-298A-488	Sequence 488, App
43	1667	90.2	345	10	US-09-978-188A-488	Sequence 488, App
44	1667	90.2	345	10	US-09-978-681A-488	Sequence 488, App
45	1667	90.2	345	10	US-09-978-194A-488	Sequence 488, App

ALIGNMENTS

RESULT 1
US-09-823-033-4
; Sequence 4, Application US/09823033
; Patent No. US20020004225A1
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE
; FILE REFERENCE: 00-12
; CURRENT APPLICATION NUMBER: US/09/823.033
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-823-033-4

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Qy	61	PKPHTYPRNVLVRLVAVDEN	VRILQITFDERGLEDPEDDICKYDFVEE	PSDGSVL	120		
Db	61	PKPHTYPRNVLVRLVAVDEN	VRILQITFDERGLEDPEDDICKYDFVEE	PSDGSVL	120		
Qy	121	GRWCGSTVPKQTSKGNHRI	RVSDEYPPSPGFCIHYSIIMPQV	TETTSVSPVLPSS	180		
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RESULT 2
US-09-818-943-2
; Sequence 2, Application US/09818943
; Patent No. US20020049987A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: LI, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: AASE, Karin
; APPLICANT: LI, Hong
; TITLE OF INVENTION: NON-HUMAN TRANSGENIC ANIMALS EXPRESSING PLATELET-DERIVED GROWTH FACTOR C, DNA CODING
; FILE REFERENCE: 1064/48487
; CURRENT APPLICATION NUMBER: US/09/818,943
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/192,507
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-818-943-2

Query Match 100.0%; Score 1848; DB 9; Length 345;
Best Local Similarity 100.0%; Pred. No. 1.2e-166;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 PKFPHYPRNMVWRLVAVDENVRIQLTFDERFGLDPEDDICKYDFVEVEEPSDGSVL 120
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RESULT 3
US-09-852-209A-7
; Sequence 7, Application US/09852209A
; Patent No. US20020164687A1
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; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; APPLICANT: BETSHOLTZ, Christer
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING
; FILE REFERENCE: 09-410349-Eriksson et al-1064-44740
; CURRENT APPLICATION NUMBER: US/09/852,209A
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/410,349
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 60/110,749
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: 60/113,002
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 60/135,426
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 60/144,022
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 39
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; SEQ ID NO 7
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-852-209A-7

Query Match 100.0%; Score 1848; DB 9; Length 345;
Best Local Similarity 100.0%; Pred. No. 1.2e-166;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 241 LKEEVKLYSCTPRNFSVSIRELKTDTTFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
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RESULT 4
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; Sequence 35, Application US/09876813
; Publication No. US20040002140A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/876,813
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Query Match 100.0%; Score 1848; DB 11; Length 345;
Best Local Similarity 100.0%; Pred. No. 1.2e-166;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-10-139-583-43
; Sequence 43, Application US/10139583
; Publication No. US20020177193A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/10/139,583
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 09/457,066
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-139-583-43

Query Match 100.0%; Score 1848; DB 13; Length 345;

Best Local Similarity 100.0%; Pred. No. 1.2e-166;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLTTSALAGQRTGTRAESNLSSKQLQSSDKQNGVQDPRHERVVTISGNGSIHS 60
DB 1 MLLGLLLTTSALAGQRTGTRAESNLSSKQLQSSDKQNGVQDPRHERVVTISGNGSIHS 60

QY 61 PKFPHYPRNMVWRLVAVDENVRILQTFDERFGLDEPDDICKYDFVEVEEPSDGSYL 120
DB 61 PKFPHYPRNMVWRLVAVDENVRILQTFDERFGLDEPDDICKYDFVEVEEPSDGSYL 120

QY 121 GRWCGSGTVPKQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
DB 121 GRWCGSGTVPKQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180

QY 181 LSLLDNNNAVAFSTLEELIRYLEPDRWQVLDLSYKPTWLLGKAFLYGKSKVVNML 240
DB 181 LSLLDNNNAVAFSTLEELIRYLEPDRWQVLDLSYKPTWLLGKAFLYGKSKVVNML 240

QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
DB 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300

QY 301 VTKKYHEVLQRPKTVGKGLHLSLTDVALEHHEBCDCVCRNAGG 345
DB 301 VTKKYHEVLQRPKTVGKGLHLSLTDVALEHHEBCDCVCRNAGG 345

RESULT 6
US-10-131-600-7
; Sequence 7, Application US/10131600
; Publication No. US20030082670A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; APPLICANT: BETHSHOUTZ, Christer
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING
; FILE REFERENCE: 09-410349-Eriksson et al-1064-44740
; CURRENT APPLICATION NUMBER: US/10/131,600
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US/09/410,349
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 60/108,109
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: 60/110,749
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: 60/113,002
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 60/135,426
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 60/144,022
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-10-131-600-7

Query Match 100.0%; Score 1848; DB 14; Length 345;
Best Local Similarity 100.0%; Pred. No. 1.2e-166;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLTTSALAGQRTGTRAESNLSSKQLQSSDKQNGVQDPRHERVVTISGNGSIHS 60
DB 1 MLLGLLLTTSALAGQRTGTRAESNLSSKQLQSSDKQNGVQDPRHERVVTISGNGSIHS 60

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Db 1 MLLGLLLLTALAGORTGTRAESNLSKQLSSDKEQNGVDP RHERVVTISGNGSIHS 60
QY 61 PKFPHTYPRNMVLVWRLVAVDENVR IQLTFDERFGLDEPDDICKYDFVEVEEPSDGSVL 120
Db 61 PKFPHTYPRNMVLVWRLVAVDENVR IQLTFDERFGLDEPDDICKYDFVEVEEPSDGSVL 120
QY 121 GRWCGSGTVPKGKTSKGNHIRFVSDEYFPSEPGFCIHYSIIMPQVTTTSPSVLPPSS 180
Db 121 GRWCGSGTVPKGKTSKGNHIRFVSDEYFPSEPGFCIHYSIIMPQVTTTSPSVLPPSS 180
QY 181 LSLDLNNAVTAFTSTLEELIRYLEPDRWQVDLSLYKPTWQLLKAFLYGKSKVNNLNL 240
Db 181 LSLDLNNAVTAFTSTLEELIRYLEPDRWQVDLSLYKPTWQLLKAFLYGKSKVNNLNL 240
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPRK 300
Db 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPRK 300
QY 301 VTKKYHEVLQLRPKTGKGLHKS LTDVALEHHEECDCVCRGNAGG 345
Db 301 VTKKYHEVLQLRPKTGKGLHKS LTDVALEHHEECDCVCRGNAGG 345
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RESULT 7

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US-10-264-361-4
; Sequence 4, Application US/10264361
; Publication No. US20030087870A1
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHOD OF TREATING FIBROSIS
; FILE REFERENCE: 00-53
; CURRENT APPLICATION NUMBER: US/10/264,361
; PRIOR FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: US/09/695,121
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-264-361-4
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```
Query Match 100.0%; Score 1848; DB 14; Length 345;
Best Local Similarity 100.0%; Pred. No. 1.2e-166;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MLLGLLLLTALAGORTGTRAESNLSKQLSSDKEQNGVDP RHERVVTISGNGSIHS 60
Db 1 MLLGLLLLTALAGORTGTRAESNLSKQLSSDKEQNGVDP RHERVVTISGNGSIHS 60
QY 61 PKFPHTYPRNMVLVWRLVAVDENVR IQLTFDERFGLDEPDDICKYDFVEVEEPSDGSVL 120
Db 61 PKFPHTYPRNMVLVWRLVAVDENVR IQLTFDERFGLDEPDDICKYDFVEVEEPSDGSVL 120
QY 121 GRWCGSGTVPKGKTSKGNHIRFVSDEYFPSEPGFCIHYSIIMPQVTTTSPSVLPPSS 180
Db 121 GRWCGSGTVPKGKTSKGNHIRFVSDEYFPSEPGFCIHYSIIMPQVTTTSPSVLPPSS 180
QY 181 LSLDLNNAVTAFTSTLEELIRYLEPDRWQVDLSLYKPTWQLLKAFLYGKSKVNNLNL 240
Db 181 LSLDLNNAVTAFTSTLEELIRYLEPDRWQVDLSLYKPTWQLLKAFLYGKSKVNNLNL 240
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPRK 300
Db 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPRK 300
QY 301 VTKKYHEVLQLRPKTGKGLHKS LTDVALEHHEECDCVCRGNAGG 345
Db 301 VTKKYHEVLQLRPKTGKGLHKS LTDVALEHHEECDCVCRGNAGG 345
```

RESULT 8

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US-10-303-997B-7
; Sequence 7, Application US/10303997B
; Publication No. US20030211994A1
; GENERAL INFORMATION:
; APPLICANT: Li, Xuri
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: CARMEIJET, Peter
; APPLICANT: COLLUM, Desire
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR MODULATING VASCULOGENESIS AND ANGIOGEN
; FILE REFERENCE: 029065.44740C3
; CURRENT APPLICATION NUMBER: US/10/303,997B
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: US 09/410,349
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: US 60/102,461
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: US 60/108,109
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/110,749
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: US 60/113,002
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: US 60/135,426
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: US 60/144,022
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 7
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-10-303-997B-7
```

```
Query Match 100.0%; Score 1848; DB 15; Length 345;
Best Local Similarity 100.0%; Pred. No. 1.2e-166;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MLLGLLLLTALAGORTGTRAESNLSKQLSSDKEQNGVDP RHERVVTISGNGSIHS 60
Db 1 MLLGLLLLTALAGORTGTRAESNLSKQLSSDKEQNGVDP RHERVVTISGNGSIHS 60
QY 61 PKFPHTYPRNMVLVWRLVAVDENVR IQLTFDERFGLDEPDDICKYDFVEVEEPSDGSVL 120
Db 61 PKFPHTYPRNMVLVWRLVAVDENVR IQLTFDERFGLDEPDDICKYDFVEVEEPSDGSVL 120
QY 121 GRWCGSGTVPKGKTSKGNHIRFVSDEYFPSEPGFCIHYSIIMPQVTTTSPSVLPPSS 180
Db 121 GRWCGSGTVPKGKTSKGNHIRFVSDEYFPSEPGFCIHYSIIMPQVTTTSPSVLPPSS 180
QY 181 LSLDLNNAVTAFTSTLEELIRYLEPDRWQVDLSLYKPTWQLLKAFLYGKSKVNNLNL 240
Db 181 LSLDLNNAVTAFTSTLEELIRYLEPDRWQVDLSLYKPTWQLLKAFLYGKSKVNNLNL 240
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPRK 300
Db 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPRK 300
QY 301 VTKKYHEVLQLRPKTGKGLHKS LTDVALEHHEECDCVCRGNAGG 345
Db 301 VTKKYHEVLQLRPKTGKGLHKS LTDVALEHHEECDCVCRGNAGG 345
```

RESULT 9

```
US-10-664-432-4
; Sequence 4, Application US/10664432
; Publication No. US20040043031A1
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE
; FILE REFERENCE: 00-12
```

```
; CURRENT APPLICATION NUMBER: US/10/664,432
; CURRENT FILING DATE: 2003-09-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-664-432-4

Query Match      100.0%; Score 1848; DB 15; Length 345;
Best Local Similarity 100.0%; Pred. No. 1.2e-166;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLTTSALAGORTGTRAESNLSSKQLSSDKEQNGVQDPRHERVVTISGNGSIHS 60
Db 1 MLLGLLLTTSALAGORTGTRAESNLSSKQLSSDKEQNGVQDPRHERVVTISGNGSIHS 60
QY 61 PKPHTYPRNMVWRLVAVDENVRILQITFDERFGLDEPDDICKYDFVEVEEPSDGSVL 120
Db 61 PKPHTYPRNMVWRLVAVDENVRILQITFDERFGLDEPDDICKYDFVEVEEPSDGSVL 120
QY 121 GRWCGSGTVPKQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
Db 121 GRWCGSGTVPKQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
QY 181 LSLDLLNNAVTAFTLEELIRYLEPDRWQVLDLSLYKPTWQLLKAFLYGKSKVNNLNL 240
Db 181 LSLDLLNNAVTAFTLEELIRYLEPDRWQVLDLSLYKPTWQLLKAFLYGKSKVNNLNL 240
QY 241 LKEEVLYSCTPRNFSVSIIRBELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
Db 241 LKEEVLYSCTPRNFSVSIIRBELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
QY 301 VTKYKHEVLQRPKTVGKGLHKSITDVALEHHEECDCVCRGNAGG 345
Db 301 VTKYKHEVLQRPKTVGKGLHKSITDVALEHHEECDCVCRGNAGG 345

RESULT 10
US-10-439-337A-7
; Sequence 7, Application US/10439337A
; Publication No. US20040053837A1
; GENERAL INFORMATION:
; APPLICANT: LI, Xuri
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: CARMELET, Peter
; APPLICANT: COLLUM, Desire
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR MODULATING VASCULOGENESIS AND
; FILE REFERENCE: 029065.44740C4
; CURRENT APPLICATION NUMBER: US/10/439,337A
; CURRENT FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: US 10/303,997
; PRIOR FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: US 09/410,349
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: US 60/102,461
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: US 60/108,109
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/110,749
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: US 60/113,002
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: US 60/135,426
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: US 60/144,022
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 345
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; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-10-439-337A-7

Query Match      100.0%; Score 1848; DB 15; Length 345;
Best Local Similarity 100.0%; Pred. No. 1.2e-166;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLTTSALAGORTGTRAESNLSSKQLSSDKEQNGVQDPRHERVVTISGNGSIHS 60
Db 1 MLLGLLLTTSALAGORTGTRAESNLSSKQLSSDKEQNGVQDPRHERVVTISGNGSIHS 60
QY 61 PKPHTYPRNMVWRLVAVDENVRILQITFDERFGLDEPDDICKYDFVEVEEPSDGSVL 120
Db 61 PKPHTYPRNMVWRLVAVDENVRILQITFDERFGLDEPDDICKYDFVEVEEPSDGSVL 120
QY 121 GRWCGSGTVPKQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
Db 121 GRWCGSGTVPKQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
QY 181 LSLDLLNNAVTAFTLEELIRYLEPDRWQVLDLSLYKPTWQLLKAFLYGKSKVNNLNL 240
Db 181 LSLDLLNNAVTAFTLEELIRYLEPDRWQVLDLSLYKPTWQLLKAFLYGKSKVNNLNL 240
QY 241 LKEEVLYSCTPRNFSVSIIRBELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
Db 241 LKEEVLYSCTPRNFSVSIIRBELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
QY 301 VTKYKHEVLQRPKTVGKGLHKSITDVALEHHEECDCVCRGNAGG 345
Db 301 VTKYKHEVLQRPKTVGKGLHKSITDVALEHHEECDCVCRGNAGG 345

RESULT 11
US-10-664-432-4
; Sequence 4, Application US/10664432
; Publication No. US20040228870A9
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE
; FILE REFERENCE: 00-12
; CURRENT APPLICATION NUMBER: US/10/664,432
; CURRENT FILING DATE: 2003-09-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-664-432-4

Query Match      100.0%; Score 1848; DB 16; Length 345;
Best Local Similarity 100.0%; Pred. No. 1.2e-166;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLTTSALAGORTGTRAESNLSSKQLSSDKEQNGVQDPRHERVVTISGNGSIHS 60
Db 1 MLLGLLLTTSALAGORTGTRAESNLSSKQLSSDKEQNGVQDPRHERVVTISGNGSIHS 60
QY 61 PKPHTYPRNMVWRLVAVDENVRILQITFDERFGLDEPDDICKYDFVEVEEPSDGSVL 120
Db 61 PKPHTYPRNMVWRLVAVDENVRILQITFDERFGLDEPDDICKYDFVEVEEPSDGSVL 120
QY 121 GRWCGSGTVPKQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
Db 121 GRWCGSGTVPKQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
QY 181 LSLDLLNNAVTAFTLEELIRYLEPDRWQVLDLSLYKPTWQLLKAFLYGKSKVNNLNL 240
Db 181 LSLDLLNNAVTAFTLEELIRYLEPDRWQVLDLSLYKPTWQLLKAFLYGKSKVNNLNL 240
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QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECCVPRK 300
Db |||||
241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECCVPRK 300
QY 301 VTKKYHEVLQLRPKTGKGLHSLTDVALEHHEEDCDVCRGNAGG 345
Db |||||
301 VTKKYHEVLQLRPKTGKGLHSLTDVALEHHEEDCDVCRGNAGG 345

RESULT 12

US-10-877-623-35
; Sequence 35, Application US/10877623
; Publication No. US20040242850A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/10/877,623
; CURRENT FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US/09/876,813
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US/09/564,595
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-877-623-35

Query Match 100.0%; Score 1848; DB 16; Length 345;
Best Local Similarity 100.0%; Pred. No. 1.2e-166;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLTSALAGORTGTRAESNLSSKQLQSSDKQNGVQDPRHVRVTTISNGSIHS 60
Db |||||
1 MLLGLLLTSALAGORTGTRAESNLSSKQLQSSDKQNGVQDPRHVRVTTISNGSIHS 60
QY 61 PKFPHTYPRNMVWLVRLVAVDENVRILQTFDERFGLDEPDDICKYDFVEVEEPSDGSVL 120
Db |||||
61 PKFPHTYPRNMVWLVRLVAVDENVRILQTFDERFGLDEPDDICKYDFVEVEEPSDGSVL 120
QY 121 GRWCSGTVPGKQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
Db |||||
121 GRWCSGTVPGKQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
QY 181 LSLDLNNAVTAFSTLEELIRYLEPDRWQVLDLSLYKPTWLLGKAFLYGKSKVVNLNL 240
Db |||||
181 LSLDLNNAVTAFSTLEELIRYLEPDRWQVLDLSLYKPTWLLGKAFLYGKSKVVNLNL 240
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECCVPRK 300
Db |||||
241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECCVPRK 300
QY 301 VTKKYHEVLQLRPKTGKGLHSLTDVALEHHEEDCDVCRGNAGG 345
Db |||||
301 VTKKYHEVLQLRPKTGKGLHSLTDVALEHHEEDCDVCRGNAGG 345

RESULT 13

US-10-938-375-4
; Sequence 4, Application US/10938375
; Publication No. US20050049218A1
; GENERAL INFORMATION:

; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHOD OF TREATING FIBROSIS
; FILE REFERENCE: 00-53
; CURRENT APPLICATION NUMBER: US/10/938,375
; CURRENT FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: US/09/695,121
; PRIOR FILING DATE: 2000-10-23
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-938-375-4

Query Match 100.0%; Score 1848; DB 17; Length 345;
Best Local Similarity 100.0%; Pred. No. 1.2e-166;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLTSALAGORTGTRAESNLSSKQLQSSDKQNGVQDPRHVRVTTISNGSIHS 60
Db |||||
1 MLLGLLLTSALAGORTGTRAESNLSSKQLQSSDKQNGVQDPRHVRVTTISNGSIHS 60
QY 61 PKFPHTYPRNMVWLVRLVAVDENVRILQTFDERFGLDEPDDICKYDFVEVEEPSDGSVL 120
Db |||||
61 PKFPHTYPRNMVWLVRLVAVDENVRILQTFDERFGLDEPDDICKYDFVEVEEPSDGSVL 120
QY 121 GRWCSGTVPGKQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
Db |||||
121 GRWCSGTVPGKQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
QY 181 LSLDLNNAVTAFSTLEELIRYLEPDRWQVLDLSLYKPTWLLGKAFLYGKSKVVNLNL 240
Db |||||
181 LSLDLNNAVTAFSTLEELIRYLEPDRWQVLDLSLYKPTWLLGKAFLYGKSKVVNLNL 240
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECCVPRK 300
Db |||||
241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECCVPRK 300
QY 301 VTKKYHEVLQLRPKTGKGLHSLTDVALEHHEEDCDVCRGNAGG 345
Db |||||
301 VTKKYHEVLQLRPKTGKGLHSLTDVALEHHEEDCDVCRGNAGG 345

RESULT 14

US-11-021-088-43
; Sequence 43, Application US/11021088
; Publication No. US20050159358A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60C1
; CURRENT APPLICATION NUMBER: US/11/021,088
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: US/09/541,752
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-021-088-43

Query Match 100.0%; Score 1848; DB 20; Length 345;
Best Local Similarity 100.0%; Pred. No. 1.2e-166;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLLLGLLLLT	SALAGORTG	TBAESNL	SSKLOI	SSDKQNG	VQDPRH	RVVTIS	NGSGSIHS	60							
Db	1	MLLLGLLLLT	SALAGORTG	TBAESNL	SSKLOI	SSDKQNG	VQDPRH	RVVTIS	NGSGSIHS	60							
Qy	61	PKFPHYTPRN	MVLVWRL	VAVDEN	VRIQLT	FDERTGLE	DPEDD	ICKYDF	VEVEPSPG	SVL120							
Db	61	PKFPHYTPRN	MVLVWRL	VAVDEN	VRIQLT	FDERTGLE	DPEDD	ICKYDF	VEVEPSPG	SVL120							
Qy	121	GRWCGSGT	VGKQTSG	KGNHIR	IRFVS	DYFSP	SEPGFC	IIHYSI	IMPQVTT	TSPSVLP	PPSS180						
Db	121	GRWCGSGT	VGKQTSG	KGNHIR	IRFVS	DYFSP	SEPGFC	IIHYSI	IMPQVTT	TSPSVLP	PPSS180						
Qy	181	LSLDLNN	AVTAF	STLEEL	IRVLE	PDQW	DLDSLY	KPTW	QLGK	AFLYG	KSKSVNNL	240					
Db	181	LSLDLNN	AVTAF	STLEEL	IRVLE	PDQW	DLDSLY	KPTW	QLGK	AFLYG	KSKSVNNL	240					
Qy	241	LKEEVK	LYSCTPR	NSVSIR	BEEL	KETDTI	FWPG	CLLV	KRCG	CNCAC	CLHNC	ECQC	VP	PK300			
Db	241	LKEEVK	LYSCTPR	NSVSIR	BEEL	KETDTI	FWPG	CLLV	KRCG	CNCAC	CLHNC	ECQC	VP	PK300			
Qy	301	VTYK	YHEVLQ	LBP	KTVG	VLH	KS	LT	DV	AL	EH	HE	BC	DV	CR	GN	AG345
Db	301	VTYK	YHEVLQ	LBP	KTVG	VLH	KS	LT	DV	AL	EH	HE	BC	DV	CR	GN	AG345

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RESULT 15
US-11-080-803-35
; Sequence 35, Application US/11080803
; Publication No. US20050164937A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGFP4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/11/080,803
; CURRENT FILING DATE: 2005-03-15
; PRIORITY APPLICATION NUMBER: US/09/876,813
; PRIORITY FILING DATE: 2001-06-06
; PRIORITY APPLICATION NUMBER: US 60/132,250
; PRIORITY FILING DATE: 1999-05-03
; PRIORITY APPLICATION NUMBER: US 60/164,463
; PRIORITY FILING DATE: 1999-11-10
; PRIORITY APPLICATION NUMBER: US 60/180,169
; PRIORITY FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-080-803-35

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	Query Match	100.0%	Score 1848	DB 20	Length 345
	Best Local Similarity	100.0%	Prod. No. 1.2e-166		
	Matches 345	Conservative 0	Mismatches 0	Indels 0	Gaps 0
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Db	1	MLLGLLLLT	SALAGQRTG	TAEENLSK	LQLSSDKEQGVQDPRHERVVTISGNGSIHS 60
Qy	61	PKPHTYPRNNVL	WRRLVAVD	ENVRIOLT	TFDERFGLGEDPEDDICKYDFEVEEFPDGSVL 120
Db	61	PKPHTYPRNNVL	WRRLVAVD	ENVRIOLT	TFDERFGLGEDPEDDICKYDFEVEEFPDGSVL 120
Qy	121	GRWCGSTVPGKQTS	KGNHIRIR	FVSDEYFPSEPGFCIHYSI	IMPQVTETTSPSVLPDSS 180
Db	121	GRWCGSTVPGKQTS	KGNHIRIR	FVSDEYFPSEPGFCIHYSI	IMPQVTETTSPSVLPDSS 180
Qy	181	LSDDLNNAVTAF	STLEELIRY	LEFDRMQVD	LDLSLYKPTWQLLGKAFLYGKKSKVNLNL 240

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181  LSLELLNNAVTAFTSLBELIRYLEPDRQVOLDLSLYKFTWQLLGKAFIYGGKSKVNLNL 240
Qy  241  LKEEVKLYSCTPRNFVSIRBELKRTDTI FWPGCILVVRCGNCACCLHNCNECCVPRK 300
241  LKEEVKLYSCTPRNFVSIRBELKRTDTI FWPGCILVVRCGNCACCLHNCNECCVPRK 300
Qy  301  VTKYHEVQLRPKTKGVKLHLSLTDVALEHHEECDCVCRGNAGG 345
Db  301  VTKYHEVQLRPKTKGVKLHLSLTDVALEHHEECDCVCRGNAGG 345

Search completed: September 3, 2005, 19:35:30
Job time : 111.5 secs

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